

Thu Apr 29 08:44:17 2004

us-10-669-689-1.rnpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2004, 16:16:37 ; Search time 1217 Seconds

(without alignments)
11573.501 Million cell updates/sec

Title: US-10-669-689-1

Sequence: 1 tccgccccgcgcggggtg.....aaaaaaaaaaaaaaaa 3124

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3124	100.0	3124	US-10-669-689-1	Sequence 1, Appl
2	3124	100.0	3124	US-10-153-921-1	Sequence 1, Appl
3	3000.8	96.1	3017	US-10-258-106-35	Sequence 35, Appl
4	2791.2	89.3	2840	US-10-037-270-20	Sequence 20, Appl
5	2791.2	89.3	2840	US-10-117-722-20	Sequence 20, Appl
6	2780.8	89.0	2895	US-10-425-114-26867	Sequence 26867, A
7	2773.8	88.8	2880	US-10-425-114-26849	Sequence 26849, A
8	2709.2	86.7	3236	US-10-425-114-26958	Sequence 26958, A
9	2595.2	83.1	2747	US-10-037-270-19	Sequence 19, Appl
10	2595.2	83.1	2747	US-10-117-722-19	Sequence 19, Appl
11	2283.4	73.1	2297	US-09-797-039-1	Sequence 1, Appl
12	2283.4	73.1	2297	US-10-423-543-18	Sequence 18, Appl
13	2283.4	73.1	2297	US-10-170-789-1	Sequence 1, Appl
14	1876.6	60.1	3915	US-09-764-868-1378	Sequence 1378, Ap

15	1876.6	60.1	7542	13	US-10-669-689-3	Sequence 3, Appl
16	1876.6	60.1	7542	13	US-10-153-921-3	Sequence 3, Appl
17	1617	51.8	1703	16	US-10-085-198-5	Sequence 5, Appl
18	1504.4	48.2	1506	13	US-10-423-543-20	Sequence 20, Appl
19	1501.4	48.1	1503	9	US-09-797-039-3	Sequence 3, Appl
20	1501.4	48.1	1503	15	US-10-170-789-3	Sequence 3, Appl
21	936.4	30.0	1069	15	US-09-933-767-74	Sequence 74, Appl
22	936.4	30.0	1069	13	US-10-004-860-74	Sequence 74, Appl
23	936.4	30.0	1069	15	US-10-023-282-74	Sequence 74, Appl
24	850	27.2	862	13	US-09-823-245-520	Sequence 520, Appl
25	593.6	19.0	727	11	US-09-764-875-127	Sequence 127, Appl
26	497.8	15.9	658	9	US-09-764-868-219	Sequence 219, Appl
27	497.8	15.9	658	11	US-09-764-875-437	Sequence 437, Appl
28	464	14.9	544	13	US-10-296-115-22	Sequence 22, Appl
29	412.4	13.2	460	10	US-09-918-995-1367	Sequence 1367, Appl
30	265.8	8.5	1480	15	US-10-204-041-9	Sequence 9, Appl
31	265.8	8.5	1480	16	US-10-305-720-1454	Sequence 1454, Appl
32	258	8.3	264	16	US-10-305-720-543	Sequence 543, Appl
33	254.8	8.2	1452	13	US-10-425-114-26649	Sequence 26649, A
34	252.6	8.1	1584	13	US-10-302-172-205	Sequence 205, Appl
35	249.2	8.0	1694	15	US-10-355-975-3	Sequence 3, Appl
36	249	8.0	1458	10	US-09-735-138-5	Sequence 5, Appl
37	244.8	7.8	1661	16	US-10-358-106-29	Sequence 29, Appl
38	244.8	7.8	1733	15	US-10-037-270-526	Sequence 526, Appl
39	244.8	7.8	1733	16	US-10-117-722-526	Sequence 526, Appl
40	244.8	7.8	1736	16	US-10-258-106-20	Sequence 20, Appl
41	244.8	7.8	1772	15	US-10-024-036B-1	Sequence 1, Appl
42	243.6	7.8	1383	10	US-09-935-664-2	Sequence 2, Appl
43	243.6	7.8	1383	15	US-10-125-835-2	Sequence 2, Appl
44	243.6	7.8	1738	10	US-09-935-464-4	Sequence 4, Appl
45	243.6	7.8	1738	15	US-10-125-835-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-669-689-1
; Sequence 1, Application US/10669689
; Publication No. US20040038632A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00612DVIIT
; CURRENT APPLICATION NUMBER: US/10/669,689
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-689-1
Query Match 100.0%; Score 3124; DB 13; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCCCGCGCGCGGCTGCGAATCCGATCCGCGCAAGCGGCTGCGCATCTGGAGGTT 60
DB 1 TCCGCCCGCGCGCGGCTGCGAATCCGATCCGCGCAAGCGGCTGCGCATCTGGAGGTT 60
QY 61 CCGTAGCCGAGACGGGCTGCTGCGCGCGGCTGCGCGCGGCTGCGCGGCTGCGCGGCTGCT 120
DB 61 CCGTAGCCGAGACGGGCTGCTGCGCGCGGCTGCGCGCGGCTGCGCGGCTGCGCGGCTGCT 120
QY 121 GCCCGCGCGCGCGGCGGCG 180

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DB 2341 GAGGAGAGAGCTTCATTTTGTCTTCTTAAGACCTGTATTTGTATTTCTG 2400
QY 2401 CTTTCCGAGTCTGCAAGTGGGCTGCTTACCTTGAACCTCATAGGCTCTAAGGAA 2460
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QY 2521 CAGTGTCCAGCTTACTGAGGCTCTTACCTTGGAGCCAAAGAGGAGGCTGATCTCT 2580
DB 2521 CAGTGTCCAGCTTACTGAGGCTCTTACCTTGGAGCCAAAGAGGAGGCTGATCTCT 2580
QY 2581 TGCTCTTCTAGATGCCACCTCTTACATCTGAGCCCAAGTCTTCTTCCACCTTAAAGG 2640
DB 2581 TGCTCTTCTAGATGCCACCTCTTACATCTGAGCCCAAGTCTTCTTCCACCTTAAAGG 2640
QY 2641 GGCTTCTGATGCAATTAATCTATATCTGATTTGGAGGTTGCCCTTTACAGGGCAG 2700
DB 2641 GGCTTCTGATGCAATTAATCTATATCTGATTTGGAGGTTGCCCTTTACAGGGCAG 2700
QY 2701 ATTTTCTGCTCAGTTCACATGAATGAAGAGGAACTCCCTCTTCTTACAGTCACTTC 2760
DB 2701 ATTTTCTGCTCAGTTCACATGAATGAAGAGGAACTCCCTCTTCTTACAGTCACTTC 2760
QY 2761 TATCAGAGGCCAGAGTCTCAGAGCCACATGAGTGTCTTTTCTGGATGAGAGTAA 2820
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DB 2821 GGGTAAATCTCCAGATTTCTTGAAGAGGCTCTGACAGGTCCTTTGTCAAGCCCTA 2880
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DB 2881 CCAAGCTGATAGGAGGCACTTGTCTCTGCTTGTCTGCGCACTCCGTGTGTGTC 2940
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DB 2941 CTGCTTCTTCTGCAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3000
QY 3001 TGTGTGCTACTGAACTGCGCAATTAACATCACTGCAAGGCAAGGCAAGGCAAGGCA 3060
DB 3001 TGTGTGCTACTGAACTGCGCAATTAACATCACTGCAAGGCAAGGCAAGGCAAGGCA 3060
QY 3061 AA 3120
DB 3061 AA 3120
QY 3121 AAAA 3124
DB 3121 AAAA 3124

RESULT 2

US-10-153-921-1

Sequence 1, Application US/10153921

Publication No. US20020142430A1

GENERAL INFORMATION:

APPLICANT: YAN Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

THEROF

FILE REFERENCE: CLO00612D1V

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/207,281

PRIOR FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 09/734,030

;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 3124
;; TYPE: DNA
;; ORGANISM: HOMO SAPIEN
US-10-153-921-1

Query Match 100.0%; Score 3124; DB 14; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCCCCGGCGGAGTGGCAATCCGGTCCGCAAGCGGCTGGCGATGCTGAGGTT 60
DB 1 TCCGCCCCCGGCGGAGTGGCAATCCGGTCCGCAAGCGGCTGGCGATGCTGAGGTT 60
QY 61 GGTAGCCGAAAGCGGCTGATCTGAGCGCGCTGCTGCCCCCGGCTGAGCGGATTTCT 120
DB 61 GGTAGCCGAAAGCGGCTGATCTGAGCGCGCTGCTGCCCCCGGCTGAGCGGATTTCT 120
QY 121 GCGGCGCGTCCCGGAGCGCTCGCGCGCGCGCTGAGCGCGGATCACTTCTCCCTGTA 180
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QY 181 CCAACCGGCGCTGAGGTTAGAGCTGAGCAATGCGGTTGGGTGTGATCTGAGCGAC 240
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QY 241 AAGAAATATATACCAAGCCATCGAGGTGACTGACATATGATTGGAGCAAGTATC 300
DB 241 AAGAAATATATACCAAGCCATCGAGGTGACTGACATATGATTGGAGCAAGTATC 300
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DB 301 AAGATGAGAGATTGTGAATCTTCCGGCCAAAGCAAGACGACAGGCAAGTGTGAC 360
QY 361 ACCCGAAGAGTTCCAGAGCGGAGCGGCAAGGTCGCAAGGCTGCCAAGACGAG 420
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QY 481 ACCCGAAGAGTACTTATCTTCTGAGCTGCGCACGCGGAGGAGGTTTGACTGG 540
DB 481 ACCCGAAGAGTACTTATCTTCTGAGCTGCGCACGCGGAGGAGGTTTGACTGG 540
QY 541 ATCTGAGCAAGGCTACTATCTGAGAGGAGCAACAAGCAAGTGTACGCAATCTCTG 600
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DB 601 GAGGCGGTGCTATTTGCACTCACTCAAGATCTGCAAGGATCTCAAGTGTGAGAAC 660
QY 661 CTGTTTACTACAACCGGCTGAAAGACTGAAATTTGATCAGTCACTTCACTGAGCT 720
DB 661 CTGTTTACTACAACCGGCTGAAAGACTGAAATTTGATCAGTCACTTCACTGAGCT 720
QY 721 AAGCTGAAATGAGCTCATCAAGGAGCCCTGTGGAGCCCGGAGTATCTGCCCCAGAG 780
DB 721 AAGCTGAAATGAGCTCATCAAGGAGCCCTGTGGAGCCCGGAGTATCTGCCCCAGAG 780
QY 781 GGTGTGCGCGGAGCGGTATGAGCGCCCTGTGAGCTGCTGGGCAATGAGTCAATGAG 840
DB 781 GGTGTGCGCGGAGCGGTATGAGCGCCCTGTGAGCTGCTGGGCAATGAGTCAATGAG 840
QY 841 TACATCTGCTTCAAGCAATCACTTCTATGAGAGGTGAGAGATATATAGAG 900
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Db	901	AACCATGATTAAGAAATCTTTCCGCAAGATCTTGGCTGGATACATAGATTGACTCTCCA	960
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QY	1021	CAAGACCAGCGGATCACTGCGAAGAGAGGCCATCTCCATGATGGAATTTCTGGCAATGCT	1080
Db	1021	CAAGACCAGCGGATCACTGCGAAGAGAGGCCATCTCCATGATGGAATTTCTGGCAATGCT	1080
QY	1081	GCTTCTGATTAAGAACATCAAGATGATGTGTCTGTGCCAAGATTGAAAAGAACTTTGCCAAG	1140
Db	1081	GCTTCTGATTAAGAACATCAAGAGATGATGTGTGTGCCAAGATTGAAAAGAACTTTGCCAAG	1140
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QY	1261	GCAAGTGGGGCACACGCTGCAGCTGCGATGAGACTACTCGAGCCTTGAGGGTATGCT	1320
Db	1261	GCAAGTGGGGCACACGCTGCAGCTGCGATGAGACTACTCGAGCCTTGAGGGTATGCT	1320
QY	1321	GCTCGTCTCTCAAGAAAGTGAATTAATGTGGCCCCGCGAACCGTATGTCACCCCAAGCACA	1380
Db	1321	GCTCGTCTCTCAAGAAAGTGAATTAATGTGGCCCCGCGAACCGTATGTCACCCCAAGCACA	1380
QY	1381	GATGGAAGTGCACACCCAGGCCACTGATGAGAGTGTCAACCCAGCCACCGATGGAAGCATC	1440
Db	1381	GATGGAAGTGCACACCCAGGCCACTGATGAGAGTGTCAACCCAGCCACCGATGGAAGCATC	1440
QY	1441	ACTCCAGCCACTGATGGAAGTGTACATCCCACTGAACAGAGCGTACTCCAGCCACT	1500
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QY	1501	GATGGGAGAGCCACACAGGCCACAGAAAGAGAGCACTGTGCCACACCCAAAGAGTGGC	1560
Db	1501	GATGGGAGAGCCACACAGGCCACAGAAAGAGAGCACTGTGCCACACCCAAAGAGTGGC	1560
QY	1561	ATGCTGGCCACCAAGAGAGCTGCCACCCCTGAGCGGCTATGCGCCAGCGGACAGCACA	1620
Db	1561	ATGCTGGCCACCAAGAGAGCTGCCACCCCTGAGCGGCTATGCGCCAGCGGACAGCACA	1620
QY	1621	GCCCCAAGGGCGCCACAGGCCAGGCTTCACCTCTAGTAAAGGGGAAAGAGGCTGTGGT	1680
Db	1621	GCCCCAAGGGCGCCACAGGCCAGGCTTCACCTCTAGTAAAGGGGAAAGAGGCTGTGGT	1680
QY	1681	TATGCCCAAGAGTCTCAAAGGAGAGGCGACGCTGAGTAAAGGCACTGTGTAAAGGGGAGG	1740
Db	1681	TATGCCCAAGAGTCTCAAAGGAGAGGCGACGCTGAGTAAAGGCACTGTGTAAAGGGGAGG	1740
QY	1741	AGGGGATGGGAGAGGGTGGGAGAGTGAATGAGGGGTTTCTCACTGATACATAAGCTCAC	1800
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QY	1801	TGGCATGATGCTTGCTCCCTCCATGCCCCACATCCCATGTGGGGCATTAAGGGGCTCA	1860
Db	1801	TGGCATGATGCTTGCTCCCTCCATGCCCCACATCCCATGTGGGGCATTAAGGGGCTCA	1860
QY	1861	CGGAGAGACATCTTGTCTCTCTGTGTGTATGTGTGTAGTGTGGGACAGGCAATGGCAG	1920
Db	1861	CGGAGAGACATCTTGTCTCTCTGTGTGTATGTGTGTAGTGTGGGACAGGCAATGGCAG	1920
QY	1921	GGCGGAGCCCAAGCCCTGATAGGATTCCTTGTGGCTTTCTGTCTTTTGTAGCTTCAAC	1980
Db	1921	GGCGGAGCCCAAGCCCTGATAGGATTCCTTGTGGCTTTCTGTCTTTTGTAGCTTCAAC	1980
QY	1981	AGTTTCTGTCTTGTGGAGTGTGCTCTAAGGATACTCAGGGGCTCTGCTCTCTTC	2040

[illegible]

Page 8

	APPLICANT: Zhang, Jie	
	TITLE OF INVENTION: Dmanac, Radoje T.	
	TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and	
	FILE REFERENCE: Polypeptides	
	CURRENT APPLICATION NUMBER: US/10/117,722	
	PRIOR FILING DATE: 2002-04-04	
	PRIOR APPLICATION NUMBER: 09/620,312	
	PRIOR FILING DATE: 2000-07-19	
	PRIOR APPLICATION NUMBER: 09/552,317	
	PRIOR FILING DATE: 2000-04-25	
	PRIOR APPLICATION NUMBER: 09/488,725	
	PRIOR FILING DATE: 2000-01-21	
	NUMBER OF SEQ ID NOS: 1104	
	SOFTWARE: pt_Fl_genes Version 1.0	
	SEQ ID NO 20	
	LENGTH: 2840	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: (206)..(1711)	
	US-10-117-722-20	
	Query Match	89.3%; Score 2791.2; DB 16; Length 2840;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 2793; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
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Db	45 TGCTGAGAGTTTCGTACCCGAAGCGCTGCATCTGGCGCGCGTCTGCCCGCGTGCTG	104
OY	110 GAGGGATTCTGCCCGCGCTTCCCAGGACCCTGGCGCCCCGCGTAGCGCGCATCACTT	169
Db	105 GAGGGATTCTGCCCGCGCTTCCCAGGACCCTGGCGCCCCGCGTAGCGCGCATCACTT	164
OY	170 CCTCCCTGTCACCAACCGCGCTGCAGTTAGAAGCTGCAATGCCGTTTGGGTGTGTA	229
Db	165 CTCTCCCTGTGACCAACCGCGCTGCAGTTAGAAGCTGCAATGCCGTTTGGGTGTGTA	224
OY	230 CTCGGGCGCACAAAGAACATAATACCAAGCCATCGAGGTGACTGAACATATGATTTGG	289
Db	225 CTCGGGCGCACAAAGAACATAATACCAAGCCATCGAGGTGACTGAACATATGATTTGG	284
OY	290 GACAGGTTCATCAAGCTGAGAGCTTTTGTGAAAATCTTCCGGGCCAAGACAAGACGACAG	349
Db	285 GACAGGTTCATCAAGCTGAGAGCTTTTGTGAAAATCTTCCGGGCCAAGACAAGACGACAG	344
OY	350 GCAAGCTGCACACCTGCAAGAGTTTCCAGAAAGCGGACGCGCAAGGTGCGGAAAGCTG	409
Db	345 GCAAGCTGCACACCTGCAAGAGTTTCCAGAAAGCGGACGCGCAAGGTGCGGAAAGCTG	404
OY	410 CCAAGAACGAGATGAGCATCTCTCAAAGTGTGAAAGCATCCCAACATCTCTACAGCTGTGG	469
Db	405 CCAAGAACGAGATGAGCATCTCTCAAAGTGTGAAAGCATCCCAACATCTCTACAGCTGTGG	464
OY	470 ATGTGTTTGTGACCCGCAAGAGATCTTATCTTCTCTGAGCTGGCCACGGGGAGGGAGG	529
Db	465 ATGTGTTTGTGACCCGCAAGAGATCTTATCTTCTCTGAGCTGGCCACGGGGAGGGAGG	524
OY	530 TGTTTGACTGATCTTGACCAAGGCTCTACTCGSAGCGAGACCAAGCAACGTGTATC	589
Db	525 TGTTTGACTGATCTTGACCAAGGCTCTACTCGSAGCGAGACCAAGCAACGTGTATC	584

Db 705 TCCATCTGCTAAGCTTAAAGAAATGGCCCTCATCAAGAGCCCTGTGGGAAACCCCGAGTATC 764
 QY 770 TGGCCCCAGAGGTGTAAGGCGCGGAGCGGTATGAGACCCCTGTGAGACTGTGGGCAATTG 829
 Db 765 TGGCCCCAGAGGTGTAAGGCGCGGAGCGGTATGAGACCCCTGTGAGACTGTGGGCAATTG 824
 QY 830 GAGTCATCATATATATCTGCTTCAAGCAATCACTCTTCTATGAGAGAGTGAAGAG 889
 Db 825 GAGTCATCATATATATCTGCTTCAAGCAATCACTCTTCTATGAGAGAGTGAAGAG 884
 QY 890 ATGATTTAGAGAACCATGATAGATGATCTCTTCCGCAAGATCCGTGGCTGTGAGCATAGAT 949
 Db 885 ATGATTTAGAGAACCATGATAGATGATCTCTTCCGCAAGATCCGTGGCTGTGAGCATAGAT 944
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 QY 1010 TGAAGGTGAGCAAGACCAAGCGGATCACTGCAAGAGAGCCATCTCCATGAGTGAATTT 1069
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 QY 1190 GGGCAACAAGACAGTCCAGCAAGGCTGAGCCAGCTGAGCTTCAAGCAAGACACTGTCCA 1249
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 QY 1250 CCCCCGGGGCTGCAAGTGGGGCCCAAGCTGAGCTGCGAGTGAAGTAACTTCAAGCCCTG 1309
 Db 1245 CCCCCGGGGCTGCAAGTGGGGCCCAAGCTGAGCTGCGAGTGAAGTAACTTCAAGCCCTG 1304
 QY 1310 AGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1369
 Db 1305 AGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1364
 QY 1370 CCCCCAGCAGATGGAAGTGCACCCAGCCCATGATGGCAGTGAACCCAGCCAGCCAG 1429
 Db 1365 CCCCCAGCAGATGGAAGTGCACCCAGCCCATGATGGCAGTGAACCCAGCCAGCCAG 1424
 QY 1430 ATGGAAGCATCTTCAGCCCATGATGGGAGTGTCAACCCAGTCACTGACAGAGCCGCTA 1489
 Db 1425 ATGGAAGCATCTTCAGCCCATGATGGGAGTGTCAACCCAGTCACTGACAGAGCCGCTA 1484
 QY 1490 CTCAAGCCTGATGGAGAGCCACACCAAGCCACAGAAAGAGAGCATGTGCTCCACCA 1549
 Db 1485 CTCAAGCCTGATGGAGAGCCACACCAAGCCACAGAAAGAGAGCATGTGCTCCACCA 1544
 QY 1550 AAAGAGTGCATGCTGTCGCAACCAAGAGTGTGCAACCCCTGAGCCGCTATGGCCAGC 1609
 Db 1545 AAAGAGTGCATGCTGTCGCAACCAAGAGTGTGCAACCCCTGAGCCGCTATGGCCAGC 1604
 QY 1610 CGGACAGACAGCCCCAGAGGGCGCCACAGGCTCAGGCTCAACCTCTAGTAAAGGGAG 1669
 Db 1605 CGGACAGACAGCCCCAGAGGGCGCCACAGGCTCAGGCTCAACCTCTAGTAAAGGGAG 1664
 QY 1670 AGGCTGCTGTTATGCTCCAGAGAGTCTCAAGAGAGAGAGCCAGGTGATGAGCAGCTGG 1729
 Db 1665 AGGCTGCTGTTATGCTCCAGAGAGTCTCAAGAGAGAGAGCCAGGTGATGAGCAGCTGG 1724
 QY 1730 TGAAGGGGGGAGAGGATGGGCAAGAGGAGTGGAGAGTGAAGAGGCTTCTCACTGTA 1789
 Db 1725 TGAAGGGGGGAGAGGATGGGCAAGAGGAGTGGAGAGTGAAGAGGCTTCTCACTGTA 1784
 QY 1790 CATAGAGTCACTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1849

Db 1785 CATAGAGTCACTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1844
 QY 1850 ACTAGGGGTCAAGGAGAGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1909
 Db 1845 ACTAGGGGTCAAGGAGAGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1904
 QY 1910 GCCAGTGGAGGGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1969
 Db 1905 GCCAGTGGAGGGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1964
 QY 1970 CTAGCTTCAACAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2029
 Db 1965 CTAGCTTCAACAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2024
 QY 2030 TGTCTCTTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 2089
 Db 2025 TGTCTCTTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 2084
 QY 2090 AACACTTCCAGAGCCCTTAACTTGGGCGGCTTGGCTGAGAGCTGTCTTCCAGAGAG 2149
 Db 2085 AACACTTCCAGAGCCCTTAACTTGGGCGGCTTGGCTGAGAGCTGTCTTCCAGAGAG 2144
 QY 2150 CCGTGTGAGGGGCTTGAAGGCTGCAATGAAGGAGTGTGCTGAGTGTGAGGAGTGTG 2209
 Db 2145 CCGTGTGAGGGGCTTGAAGGCTGCAATGAAGGAGTGTGCTGAGTGTGAGGAGTGTG 2204
 QY 2210 TCTAGAGCAGATPACAGGCTGTATAGAGATGCAAGAAAGGTAGGGCAGATATGTTAAAT 2269
 Db 2205 TCTAGAGCAGATPACAGGCTGTATAGAGATGCAAGAAAGGTAGGGCAGATATGTTAAAT 2264
 QY 2270 CCAAGCTTGGCAATAGCTAGGATATGCTCACTAGCTGTGAGAGTCTTCAAGAGTGA 2329
 Db 2265 CCAAGCTTGGCAATAGCTAGGATATGCTCACTAGCTGTGAGAGTCTTCAAGAGTGA 2324
 QY 2330 GAGATGATAGAGAGGAGAGAGCTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2389
 Db 2325 GAGATGATAGAGAGGAGAGAGCTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2384
 QY 2390 GTTATTTCTGCTTCCAGAGCTGCAAGTGGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 2449
 Db 2385 GTTATTTCTGCTTCCAGAGCTGCAAGTGGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTG 2444
 QY 2450 CTCTAAGGAAAGAGAGAACTTATAGAGCTGTGCAATGAGACCTTGCAGAGGAGAGTACA 2509
 Db 2445 CTCTAAGGAAAGAGAGAACTTATAGAGCTGTGCAATGAGACCTTGCAGAGGAGAGTACA 2504
 QY 2510 AGCCAGACCCAGATGCTCCAGCTTACTGTGCTCTTACCTTGGGCAAAAGAGAGGGC 2569
 Db 2505 AGCCAGACCCAGATGCTCCAGCTTACTGTGCTCTTACCTTGGGCAAAAGAGAGGGC 2564
 QY 2570 TGTATCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2629
 Db 2565 TGTATCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2624
 QY 2630 CCAACCTTGAAGGGCTTGTGCAATGCAATTAATCTGATTTGAGAGTGTGCTTCTTCT 2689
 Db 2625 CCAACCTTGAAGGGCTTGTGCAATGCAATTAATCTGATTTGAGAGTGTGCTTCTTCT 2684
 QY 2690 TACAGGGGAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2749
 Db 2685 TACAGGGGAGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2744
 QY 2750 CAGCTCACTTCTATCAAGGCGGCAAGTGTCTCAAGGCGGCAATTTGAGTGTCTTCTGG 2809
 Db 2745 CAGCTCACTTCTATCAAGGCGGCAAGTGTCTCAAGGCGGCAATTTGAGTGTCTTCTGG 2804
 QY 2810 ATGAGAGATGAGGTTAACTCCAGTTTCTGAG 2845
 Db 2805 ATGAGAGATGAGGTTAACTCCAGTTTCTGAG 2840


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/ Sequence 26867, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ. ID NOS: 75128
/ SEQ. ID NO 26867
/ LENGTH: 2895
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB654-060-B3_FLI
US-10-425-114-26867

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Query Match      89.0%; Score 2780.8; DB 13; Length 2895;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2885; Conservative 0; Mismatches 2; Indels 93; Gaps 1;

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QY 66 GCCGAACGGCTGCATCTGCGCGCGCTGCCCCCGCTGCTCGAGACGAAATTCGCGCG 125
DB 1 GCCGAACGGCTGCATCTGCGCGCGCTGCCCCCGCTGCTCGAGACGAAATTCGCGCG 60
QY 126 CCGTCCCCCGAGCCCTCGGCGCCCGCTGAGCCCGCGATCACTTCTCTCTGACCAAC 185
DB 61 CCGTCCCCCGAGCCCTCGGCGCCCGCTGAGCCCGCGATCACTTCTCTCTGACCAAC 120
QY 186 CCGCGCTGCAGGTAGAGCTGGAATGCGCGTTGGGTGTGTGACTCGGCGGCAAGAA 245
DB 121 CCGCGCTGCAGGTAGAGCTGGAATGCGCGTTGGGTGTGTGACTCGGCGGCAAGAA 180
QY 246 GAACTATTAACAGCCATCGAGGTGACTGACAGATATGATTTGGGACAGGTCACTAAGAC 305
DB 181 GAACTATTAACAGCCATCGAGGTGACTGACAGATATGATTTGGGACAGGTCACTAAGAC 240
QY 306 TGAAGAGTTTGTGAATCTTCCGGGCAAGCAAGACGACGAGGACCTGACACTG 365
DB 241 TGAAGAGTTTGTGAATCTTCCGGGCAAGCAAGACGACGAGGACCTGACACTG 300
QY 366 CAAGAAATTCGAAGGCGGACCGCGCAAGGTGCGGAAAGCTGCCAAGACGAGTAAAG 425
DB 301 CAAGAAATTCGAAGGCGGACCGCGCAAGGTGCGGAAAGCTGCCAAGACGAGTAAAG 360
QY 426 CATCTCAAGATGATGAGATCCCAACATCTTACAGCTGTGTGATGTGTTGTGACCGG 485
DB 361 CATCTCAAGATGATGAGATCCCAACATCTTACAGCTGTGTGATGTGTTGTGACCGG 420
QY 486 CAAGAGTACTTATCTTCTGAGAGTGCACAGGAGGAGGAGGTGTTGACTGATCTCT 545
DB 421 CAAGAGTACTTATCTTCTGAGAGTGCACAGGAGGAGGAGGTGTTGACTGATCTCT 480
QY 546 GAGACGAGGCTACTACTCGGAGGAGACACAGAACAGTGTGTCGGCAAGTCTTGAGGC 605
DB 481 GAGACGAGGCTACTACTCGGAGGAGACACAGAACAGTGTGTCGGCAAGTCTTGAGGC 540
QY 606 CGAGGCTATTTGCACTCACTCAAGATCGTGCAAGAAATCTCAAGCTGAGAGACCTGGT 665
DB 541 CGAGGCTATTTGCACTCACTCAAGATCGTGCAAGAAATCTCAAGCTGAGAGACCTGGT 600
QY 666 TTAATCAACCGGCTGAAGAACTGAAGATTGTATCATAGTCACTTCCATCTGCTAAGCT 725
DB 601 TTAATCAACCGGCTGAAGAACTGAAGATTGTATCATAGTCACTTCCATCTGCTAAGCT 660
QY 726 AGAAATGCGCTCATCAAGAGCCCTGTGGACCCCGAGTATCTGCGCCCAAGGTGT 785

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DB 661 AGAAATGCGCTCATCAAGAGCCCTGTGGACCCCGAGTATCTGCGCCCAAGGTGT 720
QY 786 AGCGCGGACGGGATGAGAGCGCCCTGTGAGCTGTGGGCGCATTTGAGTCACTGATCAT 845
DB 721 AGCGCGGACGGGATGAGAGCGCCCTGTGAGCTGTGGGCGCATTTGAGTCACTGATCAT 780
QY 846 CCGCTTTTCAAGGCAATCCACTTTCTATGAGAGGTGAGAGAGATGATTAAGAACCA 905
DB 781 CCGCTTTTCAAGGCAATCCACTTTCTATGAGAGGTGAGAGAGATGATTAAGAACCA 840
QY 906 TGAATGAATCTCTTCCGCAAGATCTGCTGTGATGATGATGATGATGATGATGATG 965
DB 841 TGAATGAATCTCTTCCGCAAGATCTGCTGTGATGATGATGATGATGATGATGATG 900
QY 966 GATGATATTTTGGAGGACCAAGACCTGTGTCAAGAGCTGATGAGGTGAGAGACAGA 1025
DB 901 GATGATATTTTGGAGGACCAAGACCTGTGTCAAGAGCTGATGAGGTGAGAGACAGA 960
QY 1026 CCAGCGGATCACTGAGAGAGGCGCATCTCCCATGATGATGATTTCTGCAATGCTGCTTC 1085
DB 961 CCAGCGGATCACTGAGAGAGGCGCATCTCCCATGATGATGATTTCTGCAATGCTGCTTC 1020
QY 1086 TGAATGAATCATCAAGAGTGTGTCTGTGCGCAATGATGAAAGAACTTTGCGAGGCGCA 1145
DB 1021 TGAATGAATCATCAAGAGTGTGTCTGTGCGCAATGATGAAAGAACTTTGCGAGGCGCA 1080
QY 1146 GTGAAGAGGCTGTCCGAGTGAACACCTCATGAAACGCTCCGGGACCAAGAGCATGTC 1205
DB 1081 GTGAAGAGGCTGTCCGAGTGAACACCTCATGAAACGCTCCGGGACCAAGAGCATGTC 1140
QY 1206 CAGACGCGCTGCAAGCGAGTGTGCTGAGCAGACGACCTGAGGCGGCGGTGAGG 1265
DB 1141 CAGACGCGCTGCAAGCGAGTGTGCTGAGCAGACGACCTGAGGCGGCGGTGAGG 1195
QY 1266 TGGGAGCACAAGCTGACAGTGTGAGTGAAGTACTGAGCCCTGAGGAGTGTGCTGCTG 1325
DB 1196 TGGGAGCACAAGCTGACAGTGTGAGTGAAGTACTGAGCCCTGAGGAGTGTGCTGCTG 1195
QY 1326 TGCTGCAAGAGTATGATGAGTGTGCGCCCGAGACCGTATGTCACCCAGCCACAGATGG 1385
DB 1196 TGCTGCAAGAGTATGATGAGTGTGCGCCCGAGACCGTATGTCACCCAGCCACAGATGG 1227
QY 1386 AAGTGCACCCGAGCCTGATGAGTGTGACCCGACCGACCGATGGAAGCATCATCC 1445
DB 1228 AAGTGCACCCGAGCCTGATGAGTGTGACCCGACCGACCGATGGAAGCATCATCC 1287
QY 1446 AGCAGCTGATGAGGAGTGTGACCCGAGTCACTGACAGGAGGCGTATCTCAAGCATGATGG 1505
DB 1288 AGCAGCTGATGAGGAGTGTGACCCGAGTCACTGACAGGAGGCGTATCTCAAGCATGATGG 1347
QY 1506 GAGAGCCACACCAAGCACAAGAGAGCACTGTGTCACCAACCAAGAGAGTGCATGCT 1565
DB 1348 GAGAGCCACACCAAGCACAAGAGAGCACTGTGTCACCAACCAAGAGAGTGCATGCT 1407
QY 1566 GGCACCAAGGCACTGCACTGAGCGGCTATGAGCCGACGAGCAGACAGCCCC 1625
DB 1408 GGCACCAAGGCACTGCACTGAGCGGCTATGAGCCGACGAGCAGACAGCCCC 1467
QY 1626 AGAGGCGCCCAAGGCGAGGTCACACCTCTATGAAAGGAGAGAGGCTGTGTTATGC 1685
DB 1468 AGAGGCGCCCAAGGCGAGGTCACACCTCTATGAAAGGAGAGAGGCTGTGTTATGC 1527
QY 1686 CCAAGAGTCTCAAAAGGAGAGGAGCAGCTGATGAGAGGAGGAGGAGGAGGAGGAGG 1745
DB 1528 CCAAGAGTCTCAAAAGGAGAGGAGCAGCTGATGAGAGGAGGAGGAGGAGGAGGAGG 1587
QY 1746 ATGGGACAGAGGAGGAGAGTGAATGAGAGGAGCTTCTCATCTGTACATGAGTCACTGGCA 1805
DB 1588 ATGGGACAGAGGAGGAGAGTGAATGAGAGGAGCTTCTCATCTGTACATGAGTCACTGGCA 1647
QY 1806 TGATGCTCTGCTCTCCCATATGCTCCCAATGCTCCCAATGCTCCCAATGCTCCCAATG 1865
DB 1648 TGATGCTCTGCTCTCCCATATGCTCCCAATGCTCCCAATGCTCCCAATGCTCCCAATG 1707

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QY 607 GTGGCTATTGGCACTCACTCAAGATGCTGCACAGAAATCTCAAGCTGGAGAACTTGTT 666
Db 541 GTGGCCATTATGGCACTCACTCAAGATGCTGCACAGAAATCTCAAGCTGGAGAACTTGTT 600
QY 667 TACTACAACGGGCTGAAGAACTGAAGATGTGTATCAAGTCACTTCCATCTGGCTAAGCTA 726
Db 601 TACTACAACGGGCTGAAGAACTGAAGATGTGTATCAAGTCACTTCCATCTGGCTAAGCTA 660
QY 727 GAAATGCTCTCAACAAGAGACCTGTGAGACCCCGAAGTATCTGGCCCAAGAGTGTGA 786
Db 661 GAAATGCTCTCAACAAGAGACCTGTGAGACCCCGAAGTATCTGGCCCAAGAGTGTGA 720
QY 787 GAGCGGACGGATGAGACCGCTGTGAGCTGTGGCCATTGAGTCACTATGATCATC 846
Db 721 GAGCGGACGGATGAGACCGCTGTGAGCTGTGGCCATTGAGTCACTATGATCATC 780
QY 847 CTGCTTCAAGGCAATCCACTTTCTATGAGAGAGTGAAGAAATGATTATGAAACCAT 906
Db 781 CTGCTTCAAGGCAATCCACTTTCTATGAGAGAGTGAAGAAATGATTATGAAACCAT 840
QY 907 GATPAAGATCTCTCCGCAAGATCTGGCTGTGATCACTATGAGTGAATCTCCATATTGG 966
Db 841 GATPAAGATCTCTCCGCAAGATCTGGCTGTGATCACTATGAGTGAATCTCCATATTGG 900
QY 967 GATGATATTTCCGAGGACGCAAGAACCTGTGCACAAAGGCTGATGAGAGTGAAGAAC 1026
Db 901 GATGATATTTCCGAGGACGCAAGAACCTGTGCACAAAGGCTGATGAGAGTGAAGAAC 960
QY 1027 CAGCGGATCACTGCAGAGAGGSCCATCTCCATGAGTGAATTTCTGCAATGCTGTTCT 1086
Db 961 CAGCGGATCACTGCAGAGAGGSCCATCTCCATGAGTGAATTTCTGCAATGCTGTTCT 1020
QY 1087 GATPAAGATCTCAAGAGTGTGTCTGTGCCCAATTTGAAGAACTTTGCGAGAGGCAAG 1146
Db 1021 GATPAAGATCTCAAGAGTGTGTCTGTGCCCAATTTGAAGAACTTTGCGAGAGGCAAG 1080
QY 1147 TGAAGAAGGCTGTCCGAGTGAACACCCCTATGAAACGGGCTCCGGGCAACAGAGCATGC 1206
Db 1081 TGAAGAAGGCTGTCCGAGTGAACACCCCTATGAAACGGGCTCCGGGCAACAGAGCATGC 1140
QY 1207 AGCAGGCTGCAGCCCAAGTGCCTCAAGCACAAGACATGTCACCCCGGGCTGTGAGGT 1266
Db 1141 AGCAGGCTGCAGCCCAAGTGCCTCAAGCACAAGACATGTCACCCCGGGCTGTGAGGT 1194
QY 1267 GGGGCAAGAGCTGCAGTGCAGTGAAGTCACTCAAGCCCTGAGGGGTGATGCTGCTGT 1326
Db 1195 ----- 1194
QY 1327 GCTGCAAGAAGTGAATATGTGGCCCGGAGACCTGATGTCACCCCAAGCACAAGTGA 1386
Db 1195 -----GAGACCTGATGTGCACCCCAAGCACAAGTGA 1227
QY 1387 AGTGCACCCCGAGCACTGATGAGAGTGTCAACCCCAAGCACAAGTGAAGATCACTTCA 1446
Db 1228 AGTGCACCCCGAGCACTGATGAGAGTGTCAACCCCAAGCACAAGTGAAGATCACTTCA 1287
QY 1447 GCCACTGATGAGAGTGTCAACCCCAAGTCACTGACAGAGAGCGCTACTCAGGCACTGATG 1506
Db 1288 GCCACTGATGAGAGTGTCAACCCCAAGTCACTGACAGAGAGCGCTACTCAGGCACTGATG 1347
QY 1507 AGAGCCACACAGCACAAGAGAGAGCATGTGTGCCACCAACCCCAAGAGTGCATGTCTG 1566
Db 1348 AGAGCCACACAGCACAAGAGAGAGCATGTGTGCCACCAACCCCAAGAGTGCATGTCTG 1407
QY 1567 GCCACCAAGGACGTGCACCCCTGAGCGGGCTATGGCCCAAGGCAAGGCAAGGCCCA 1626
Db 1408 GCCACCAAGGACGTGCACCCCTGAGCGGGCTATGGCCCAAGGCAAGGCAAGGCCCA 1467
QY 1627 GAGGCGCCACAGGCGCAGCTCCACCTCTAGTAAAGGGAGAGGCTGTGTTATGCC 1686
Db 1468 GAGGCGCCACAGGCGCAGCTCCACCTCTAGTAAAGGGAGAGAGGCTGTGTTATGCC 1527

QY 1687 CAGAGTCTCAAAGGAGAGAGGCCACGCTGAGTGAAGCAGCTGTGAGAGGGGGGCAAGGGGA 1746
Db 1528 CAGAGTCTCAAAGGAGAGAGGCCACGCTGAGTGAAGCAGCTGTGAGAGGGGGGCAAGGGGA 1587
QY 1747 TGGGAGAGAGGGGTGGAGAGTGAAGAGGGGCTCTCACTGATGATGATGATGATGATGAT 1806
Db 1588 TGGGAGAGAGGGGTGGAGAGTGAAGAGGGGCTCTCACTGATGATGATGATGATGATGAT 1647
QY 1807 GATGCGCTGCTCCCGCATGCCCCACATCCAGTGGGAGATTAATGAGGGGTCAAGGGAG 1866
Db 1648 GATGCGCTGCTCCCGCATGCCCCACATCCAGTGGGAGATTAATGAGGGGTCAAGGGAG 1707
QY 1867 AGCAGTCTGCTCTCTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1926
Db 1708 AGCAGTCTGCTCTCTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1767
QY 1927 CCCCAGCCCCGATGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1986
Db 1768 CCCCAGCCCCGATGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1827
QY 1987 TGTTCCTGT 2046
Db 1828 TGTTCCTGT 1887
QY 2047 CTTTCTTGCTCAACCATTCCTCTAGGAGGCGCTGACAGTCCCACTCTTCCAGGCGCT 2106
Db 1888 CTTTCTTGCTCAACCATTCCTCTAGGAGGCGCTGACAGTCCCACTCTTCCAGGCGCT 1947
QY 2107 AAACCTGGGCGGCTTGCTGCTGAGAGCTGTCTTCCACGAGGCGCTGTGACGCGCTTGA 2166
Db 1948 AAACCTGGGCGGCTTGCTGCTGAGAGCTGTCTTCCACGAGGCGCTGTGACGCGCTTGA 2007
QY 2167 GGGCTCTGCAATGAAGGT 2226
Db 2008 GGGCTCTGCAATGAAGGT 2067
QY 2227 GCTGTATGAGAGTGCAGAAAGGTAGGCGATGATTTAAATGTCACAGCTTGGCACATGG 2286
Db 2068 GCTGTATGAGAGTGCAGAAAGGTAGGCGATGATTTAAATGTCACAGCTTGGCACATGG 2127
QY 2287 CTAGGATACTGCTCACTAGT 2346
Db 2128 CTAGGATACTGCTCACTAGT 2187
QY 2347 CAGAACTTCAATTTTGTCTTCTTAAAGACCTGTATTTGTGTATTTTCTGCTTTC 2406
Db 2188 CAGAACTTCAATTTTGTCTTCTTAAAGACCTGTATTTGTGTATTTTCTGCTTTC 2247
QY 2407 CGAGTCTGCAAGTGGGCGCTGTACCTGAACTCATAGAGCTTAAAGGAAAGGAGG 2466
Db 2248 CGAGTCTGCAAGTGGGCGCTGTACCTGAACTCATAGAGCTTAAAGGAAAGGAGG 2307
QY 2467 AACCAATTGAGAGTGCAGATGAGACTGTGCAGGGCAGAGTAAAGCCAGACCCAGTGT 2526
Db 2308 AACCAATTGAGAGTGCAGATGAGACTGTGCAGGGCAGAGTAAAGCCAGACCCAGTGT 2367
QY 2527 CCGAGCTTACTGAGTCTTACCTGTGAGGCAAGGAGGAGGCTGATTACTCTTGTCTT 2586
Db 2368 CCGAGCTTACTGAGTCTTACCTGTGAGGCAAGGAGGAGGCTGATTACTCTTGTCTT 2427
QY 2587 TCTTGAAGAGCCACTCTCTAATCTGACCCCAAAATCTCTTCCACCCCTTAAGGGGGCTTG 2646
Db 2428 TCTTGAAGAGCCACTCTCTAATCTGACCCCAAAATCTCTTCCACCCCTTAAGGGGGCTTG 2487
QY 2647 CTGATGAGCAATTAATCTAATCTGATTTGAGAGGTTGGCTTTACAGGGGAGATTTTC 2706
Db 2488 CTGATGAGCAATTAATCTAATCTGATTTGAGAGGTTGGCTTTACAGGGGAGATTTTC 2547
QY 2707 TGTCTAGTTCAACATGAATGAAGAGAACTCCCTTTTCTACAGCTCACTTCTATCAG 2766
Db 2548 TGTCTAGTTCAACATGAATGAAGAGAACTCCCTTTTCTACAGCTCACTTCTATCAG 2607
QY 2767 AGGCCAGAGTCTCAAGAGCCACATTAAGTTGCTTTTCTGTGGATGAGAAATGAGGTTA 2826

D _b	AAGCCAGGAGCCTCAGACCAATTGAATGCCTTTTCGTGGATGAGAAATGAGGTTA	2667
Q _y	AACTCCCAGTTTCCGAGAGGAGGCCTCGACAGGTGCCCTTATCAGACCCTACACAG	2886
D _b	AACTCCCCAGTTTCCGAGGAGGAGCCTCTGACAGGTGCCCTTATGTCAGACCCACACAG	2127
Q _y	CCTGATAGGACGCCAATTGCTCTCGCCTTGCTCGGCACTCCGTGATGCTCTGCCC	2946
D _b	CCGAGATAGGACGCCCATTTGCTCTCGCCTTGCTCGGCACTCCGTGATGCTCTGCCC	2787
Q _y	TTCCTCCTGCATCCGATGGAGTCTGCTCTGAGTGTGAAGATCGATGGGTTAACTGTGTG	3006
D _b	TTCCTCCTGCATCCGATGGAGTCTGCTCTGAGTGTGAAGATCGATGGGTTAACTGTGTG	2847
Q _y	CCACTGAAACCTGGCAAATAAACATCACCCCTGC	3039
D _b	CCTAAGAACAATGCAATAAATATCCCTCTGC	2880

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; RESULT 8
; US-10-425-114-26958
; Sequence 26958: Application US/10425114
; Publication NO. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 73128
; SEQ ID NO 26958
; LENGTH: 3236
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4676-058-A2_FLI
; US-10-425-114-26958

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Query Match	86.7%	Score 2709.2	DB 13	Length 3236
Best Local Similarity	92.2%	Pred. No. 0		
Matches 2982; Conservative	0	Mismatches 3	Indels 251	Gaps 2

QY	61	CGCTAGCCGAAGCGGCTGCATCTGGGCGCGCTCTGCCCGCGTGTCCGAGCGGAATCT	120
Db	1	CGCTAGCCGAAGCGGCTGCATCTGGGCGCGCTCTGCCCGCGTGTCCGAGCGGAATCT	60
QY	121	GCCCCGCTGCCGGAGCCCTGGGCGCCCGCTGAGCCCGGATCATCTTCTCCTGTGA	180
Db	61	GCCCCGCTGCCGGAGCCCTGGGCGCCCGCTGAGCCCGGATCATCTTCTCCTGTGA	120
QY	181	CCAACCGGCGCTGACAGTTAAGACCTGGCAATGCCGTTGGGTGTGTGACTCTGGGGAC	240
Db	121	CCAACCGGCGCTGACAGTTAAGACCTGGCAATGCCGTTGGGTGTGTGACTCTGGGGAC	180
QY	241	AAGAAGACTATAACGACGCATCCGAGGTGACTGACAGATTGATTTGGGACAGGTCATC	300
Db	181	AAGAAGACTATAACGACGCATCCGAGGTGACTGACAGATTGATTTGGGACAGGTCATC	240
QY	301	AAGACTGAGGAGTTTGTGTAATCTTCCGGGCCAAGGACAAGACGACAGGCAAGCTGCAC	360
Db	241	AAGACTGAGGAGTTTGTGTAATCTTCCGGGCCAAGGACAAGACGACAGGCAAGCTGCAC	300
QY	361	ACCTGCAAGAAGTTCAGAAAGCGGGAGCGCGCCAGAGGTGCGGAAAGCTGCCAAGAGAG	420
Db	301	ACCTGCAAGAAGTTCAGAAAGCGGGAGCGCGCCAGAGGTGCGGAAAGCTGCCAAGAGAG	360

QY	421	ATAGGCAATCTCAAGATGAGGAGCATGCCAATCTCAAGCTGGGAGATGTGTGTG	480
Db	361	ATAGGCAATCTCAAGATGAGGAGCATGCCAATCTCAAGCTGGGAGATGTGTGTG	420
QY	481	ACCGGCAAGGAGTACTTTATCTTCTGGAGCTGGCCAAGGAGGAGGTGTGACTGG	540
Db	421	ACCGGCAAGGAGTACTTTATCTTCTGGAGCTGGCCAAGGAGGAGGTGTGACTGG	480
QY	541	ATCTGGAACCAAGGCTACTCTGGAGCCGAGACCAAGCAACTGTGGTACGGCAATCTGG	600
Db	481	ATCTGGAACCAAGGCTACTCTGGAGCCGAGACCAAGCAACTGTGGTACGGCAATCTGG	540
QY	601	GAGGCGGTGGCCTATTGGCACTCACTCAAGATGTTGACAGAGATCTCAAGCTGGAGAC	660
Db	541	GAGGCGGTGGCCTATTGGCACTCACTCAAGATGTTGACAGAGATCTCAAGCTGGAGAC	600
QY	661	CTGGTTTACTACAACCGGCTGAAGAACTCGAAGTTGTCTCACTGATGACTTCACTTGGCT	720
Db	601	CTGGTTTACTACAACCGGCTGAAGAACTCGAAGTTGTCTCACTGATGACTTCACTTGGCT	660
QY	721	AACTTAAGAAATGAGCTCTCATCAAGAGCCCTGTGGGACCCCGAGTATCTG-----	771
Db	661	AACTTAAGAAATGAGCTCTCATCAAGAGCCCTGTGGGACCCCGAGTATCTG-----	720
QY	772	-----	771
Db	721	GCGGTGGGCGAAGGCGGAGGAGATATGAGGAGCAAGCTTCAAGGAGCTGCTTGGGCAAG	780
QY	772	-----	771
Db	781	GCGGAAATGTGCTCATCTCAGGAAGTGGTGTGGATGTGATCTGCACTGGCTGAGGCTGG	840
QY	772	-----GCCCCAAGGTGTATGAGGCCCGCAGCGGT	799
Db	841	ATACTGACCAAGAGATGGGCGCTGTGTTGTATGAGCCCAAGAGTGTATGGCCGAGCGGT	900
QY	800	ATGGAACCCCTGTGGAATCTGTGGGCCATTGGAATCATCATGTATCACTCT-----	848
Db	901	ATGGAACCCCTGTGGAATCTGTGGGCCATTGGAATCATCATGTATCACTCTGTGATGGTACA	960
QY	849	-----	848
Db	961	GATGGAACAAGCAAGGCTTGCAGTCAAGTGGGATGGGGCAATGTGTCTGTGGCTTCTGTG	1020
QY	849	-----GCTTTCAGGCAATCCACTTTCATATGAGAGGTGGAGAG	889
Db	1021	TGAGCCCTTCCCAATGAGGCTTTCAGGCAATCCACTTTCATATGAGAGGTGGAGAG	1080
QY	890	ATGATTTATGGAACCATGATTAAGATTTCTTCGCAAGATCTGGCTGTGTGATCTATAGT	949
Db	1081	ATGATTTATGGAACCATGATTAAGATTTCTTCGCAAGATCTGGCTGTGTGATCTATAGT	1140
QY	950	TTGACTCTCCATATGAGGATGATTAATTTCGAGGAGCCAAAGACTGTGTCAAGGCTGA	1009
Db	1141	TTGACTCTCCATATGAGGATGATTAATTTCGAGGAGCCAAAGACTGTGTCAAGGCTGA	1200
QY	1010	TGAGAGTGGAGCAAGACCAAGGATCTGACAGAGAGGCAATCTCCCATGATGATTT	1069
Db	1201	TGAGAGTGGAGCAAGACCAAGGATCTGACAGAGAGGCAATCTCCCATGATGATTT	1260
QY	1070	CTGGCAATGCTGCTTCTGATTAAGAACTCAAGATGTTGTGTGTGCCAAGTTGAAAGA	1129
Db	1261	CTGGCAATGCTGCTTCTGATTAAGAACTCAAGATGTTGTGTGTGCCAAGTTGAAAGA	1320
QY	1130	ACTTTTGCAGGGCCAAATGGAAGAAAGGCTTCCGAGTGAACAACCTCATGATAAGCGGCTC	1189
Db	1321	ACTTTTGCAGGGCCAAATGGAAGAAAGGCTTCCGAGTGAACAACCTCATGATAAGCGGCTC	1380
QY	1190	GAGGACACAGAGCAAGTCCAGACCGGCTCAACCCAGTGGGCTTCAAGCCACAGACTGTCCA	1249
Db	1381	GAGGACACAGAGCAAGTCCAGACCGGCTTCAACCCAGTGGGCTTCAAGCCACAGACTGTCCA	1440
QY	1250	CCCCCGGAGCTGACAGTGGGGCCAAGCTGCAAGCTGCAAGTGAAGTAACTTCAAGCCCTTG	1309

1441 CCCCCGGGCTCAGGTGGGGCCACAGCTGCAGCTGCCAGTGAATCTACAGCCCTG 1500
QY 1310 AGGGTGAATGCTCTGCTGCAAAAGATGATATGTGGCCCCCGCAGACCGTACTGCCA 1369
Db 1501 AGGGTGAATGCTCTGCTGCAAAAGATGATATGTGGCCCCCGCAGACCGTACTGCCA 1560
QY 1370 CCCCCGACAGATGGAATGTCACCCCGCCACTGATGAGCATGTCACCCCAAGCACC 1429
Db 1561 CCCCCGACAGATGGAATGTCACCCCGCCACTGATGAGCATGTCACCCCAAGCACC 1620
QY 1430 ATGGAAGCATCACTCAGGCCACTGATGGAAGTGTACCCCACTGACTGACAGAGCGCTA 1489
Db 1621 ATGGAAGCATCACTCAGGCCACTGATGGAAGTGTACCCCACTGACTGACAGAGCGCTA 1680
QY 1490 CTCACAGCATGATGGAAGGCCACACAGCCACAGAAAGAGACCTGTGCCACACCC 1549
Db 1681 CTCACAGCATGATGGAAGGCCACACAGCCACAGAAAGAGACCTGTGCCACACCC 1740
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Db 1741 AAAGCATGTCATGTCGTCACCAAGGAGCTGCCACCCCTGAGCCGCTATGCCCCAGC 1800
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QY 1670 AGGCTCTGCTTATGCCCAGGAGTCTCAAAAGGAGGAGGCAAGCTGAGAGGAGCGTGG 1729
Db 1861 AGGCTCTGCTTATGCCCAGGAGTCTCAAAAGGAGGAGGCAAGCTGAGAGGAGCGTGG 1920
QY 1730 TGAAGGGGGGCAAGGGATGCGGAGAGGAGGAGGAGTGAAGAGGAGGCTTCTCACTGA 1789
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QY 1850 ACTAGAGGATCACGGGAGAGAGTCTGCTCTGCTGATGATGATGATGATGATGATGATG 1909
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QY 1910 GCGAGTGGAGGGGCGGCCCCAGCCCCCTGATGATGATGATGATGATGATGATGATGATG 1969
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QY 1970 CTAGCTTACCAAGTTTCTGTTCTTGTGAGATGCTGCTTGAAGGATACCTCAGGGGCTCC 2029
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QY 2090 ACACTTCCCAAGGCTTAACTTGGGCGGCTTGCCTTGAAGTGGTCTCTCAGAGGAG 2149
Db 2281 ACACTTCCCAAGGCTTAACTTGGGCGGCTTGCCTTGAAGTGGTCTCTCAGAGGAG 2240
QY 2150 CCTGTGAGCGGTCTTGAAGCTCTGACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGT 2209
Db 2341 CCTGTGAGCGGTCTTGAAGCTCTGACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGT 2400
QY 2210 TCTAGAGAGCAGATACAGGCTGTGTATGAGGATGCAAAAGTATGATGTTTAACT 2269
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QY 2330 GAGATGATGAGAGGGGAGGAGGCTTCACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2389

Db 2521 GAGATGATGAGAGGGGAGGAGGCTTCACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2580
QY 2390 GTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2449
Db 2581 GTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2640
QY 2450 CTCTAAGGAAAGAGAGGAACTATGAGACGTGCAATGAGACCTGACAGGGCAGATGACA 2509
Db 2641 CTCTAAGGAAAGAGAGGAACTATGAGACGTGCAATGAGACCTGACAGGGCAGATGACA 2700
QY 2510 AGCCAGACACCAAGTGTCCAGGCTTACTGAGGCTTACTTACCTTGGGCCAAACAGGGAGG 2569
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QY 2570 TGATACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2629
Db 2761 TGATACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2820
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Db 2821 CCAACCTAAGGGGCTTCTGTCATGAGGCAATPACTCATPACTGATTTGAGGTTTGGCCTT 2880
QY 2690 TACAGGGGAGATTTTCTGCTCAGTTCACATGAAATGAAAGAGAACTCCCTTTCTTA 2749
Db 2881 TACAGGGGAGATTTTCTGCTCAGTTCACATGAAATGAAAGAGAACTCCCTTTCTTA 2940
QY 2750 CAGCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2809
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Db 3061 GTCAAGCCCTACAGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
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QY 2990 GGTGGTTAACTGTGTGCTTACTGAACCTGGCAATTAACATCACTTGGCAAGCC 3045
Db 3181 GGTGGTTAACTGTGTGCTTACTGAACCTGGCAATTAACATCACTTGGCAAGCC 3236

RESULT 9
US-10-037-270-19
; Sequence 19, Application US/10037270
; Publication No. US20030104529A1
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungting
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radjoje T.
; TITLE OF INVENTION: No. US20030104529A1 Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270

; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/486,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1104
 ; SOFTWARE: pc_files Version 1.0
 ; SEQ ID NO: 19
 ; LENGTH: 2747
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (206)..(1618)
 ; US-10-037-270-19

Query Match 83.1%; Score 2595.2; DB 15; Length 2747;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

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 DB 45 TGCTGAGGCTTCGCTAGCGGAGGCGGCTGATCGGCGCGCGCTGCGCGGCTGCTCG 104
 QY 110 GAGCGGATTCGCGCGCGCGCTGCGGAGCGCTGCGCGCGCGCTGAGCGCGCGATCACTT 169
 DB 105 GAGCGGATTCGCGCGCGCGCTGCGGAGCGCTGCGCGCGCGCTGAGCGCGCGATCACTT 164
 QY 170 CCTCCCTGTGACCAACCGCGCGCTGAGGCTTGAAGCTTGGCAATGCGCTTGGGTGTGA 229
 DB 165 CCTCCCTGTGACCAACCGCGCGCTGAGGCTTGAAGCTTGGCAATGCGCTTGGGTGTGA 224
 QY 230 CTCTGGGCGCAAGAACTATTAACAGCCATCGAGGTGATCTGACAGATATGATTTGG 289
 DB 225 CTCTGGGCGCAAGAACTATTAACAGCCATCGAGGTGATCTGACAGATATGATTTGG 284
 QY 290 GACAGGTCATCAAGCTGAGGAGTTTGTGAATCTTCCGGGCGCAAGGACAAAGCGACAG 349
 DB 285 GACAGGTCATCAAGCTGAGGAGTTTGTGAATCTTCCGGGCGCAAGGACAAAGCGACAG 344
 QY 350 GCAAGCTGCAACCTGCAAGAGTTCCAGAGCGGAGCGCGCGAGGCGGAGAACTG 409
 DB 345 GCAAGCTGCAACCTGCAAGAGTTCCAGAGCGGAGCGCGCGAGGCGGAGAACTG 404
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 DB 405 CCAAGAACGAGATAGGACCTCTCAAGATGTGAAGCATCCCAACATCTTACAGTGTGG 464
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 DB 525 TGTTTGATGATCTGAGCAAGGCTTACTCAAGGCTGAGGAGGAGCAAGAGCAAGTGTAC 584
 QY 590 GCGAAGTCTGAGGCGCGTGGCTTATTTGCACTCACTCAAGATGCTGACAGAACTCA 649
 DB 585 GCGAAGTCTGAGGCGCGTGGCTTATTTGCACTCACTCAAGATGCTGACAGAACTCA 644
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 DB 765 TGGCCCGCAGAGGTGAGGCGGAGCGGATGAGCGCGCTGTGAGCTGCGGCGCAATG 824
 QY 830 GAGTCATCATGATCACTCTGCTTTCAGGCAATCCACTTTCTATGAGAGGTGAGAAAG 889

DB 825 GAGTCATCATGATCACTCTGCTTTCAGGCAATCCACTTTCTATGAGAGGTGAGAAAG 884
 QY 890 ATGATTAATGAGAACCATGATTAAGATCTTCCGAGATCCTGCGTGTGATATGAGT 949
 DB 885 ATGATTAATGAGAACCATGATTAAGATCTTCCGAGATCCTGCGTGTGATATGAGT 944
 QY 950 TTGACTCTTCATATTTGGGATGATATTTGCGAGGCGCAAGAACTGCTCAAGGCTGA 1009
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 QY 1010 TGGAGGTGAGCAAGACCGAGGATCACTGCAAGAGAGGAGGAGGAGGAGGAGGAGG 1069
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 QY 1070 CTGGCAATGCTGCTCTGATTAAGAACATCAAGAGATGTGTCTGCGCAGATTGAAAAG 1129
 DB 1065 CTGGCAATGCTGCTCTGATTAAGAACATCAAGAGATGTGTCTGCGCAGATTGAAAAG 1124
 QY 1130 ACTTTGCGAGGCGCAAGTGAAGAGGCTGTCCAGTGAACCACTCTCAATGAACGCTTC 1189
 DB 1125 ACTTTGCGAGGCGCAAGTGAAGAGGCTGTCCAGTGAACCACTCTCAATGAACGCTTC 1184
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 DB 1256 -----CGAGCCGTAAGTCCA 1271
 QY 1370 CCCCAAGCAGATGGAAGTGCACCCAGCCACTGATGCGAGTGCACCCAGCGACCG 1429
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 QY 1430 ATGGAAGCATCACTCCAGCCACTGATGGAAGTGTCACTCCAGTCACTGACAGAGCGCTA 1489
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 QY 1632 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1691
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 QY 1752 ACTAGAGGATCAAGGAGAGCAAGTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1811
 DB 1910 GCCAGTGGCAGGAGGCGGCGCCAGCCCTGATGATGATTTCTTGTGCTTTTGTG 1969

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Page 16

Db	1812	GCAGATGGCAGAGGGCCGGCCCCAGCCCGCTGCATGGATTCCTGTGGCTTTCTGTCTTTTG	1871
QY	1970	CTAGCTTACCAACAGTTTCTGTCTCTTGTGGGATGTGCTCTTAGGGATTACTCAGGGGGCTCC	2029
Db	1872	CTAGCTTACCAACAGTTTCTGTCTCTTGTGGGATGTGCTCTTAGGGATTACTCAGGGGGCTCC	1931
QY	2030	TGCTCTCTCCCTCCCTTCCCTCTTGGCCCTCAACATTCCTCCCTAGGAGGCGCTGCAGGTCCC	2089
Db	1932	TGCTCTCTCCCTCCCTTCCCTCTTGGCCCTCAACATTCCTCCCTAGGAGGCGCTGCAGGTCCC	1991
QY	2090	ACACTCTCCAGAGCGCTTAAACTTTGGGCGGCTTGCCCTGAGAGCTGTCTCCAGCGAGG	2149
Db	1992	ACACTCTCCAGAGCGCTTAAACTTTGGGCGGCTTGCCCTGAGAGAGTGTGTCTCCAGCGAGG	2051
QY	2150	CCCTGTACGGGCTTAAAGCTCTGCGACATGAAAGTGTGTGCTGTGTGTGGCTGC	2209
Db	2052	CCCTGTACGGGCTTAAAGCTCTGCGACATGAAAGTGTGTGCTGTGTGTGGCTGC	2111
QY	2210	TCTTAGGAGCAGATACAGGCTGTATTAGAGATGAGAAAGGTAGGGCAGTATGTTTAACT	2269
Db	2112	TCTTAGGAGCAGATACAGGCTGTATTAGAGATGAGAAAGGTAGGGCAGTATGTTTAACT	2171
QY	2270	CCAGACTTTGGCACAATGGCTAGGATATACGTCACTAGCTGTGAGAGTCTCAGAGATGGA	2329
Db	2172	CCAGACTTTGGCACAATGGCTAGGATATACGTCACTAGCTGTGAGAGTCTCAGAGATGGA	2231
QY	2330	GAGATGAGTATGAGAGGGCAGAAAGCTTCCATTTTTGTCTCTTAAAGACCTGTTATTTGT	2389
Db	2232	GAGATGAGTATGAGAGGGCAGAAAGCTTCCATTTTTGTCTCTTAAAGACCTGTTATTTGT	2291
QY	2390	GTTATTTCTGCTCTTCCGAGTCTCGAGTGGGCTGCCCTGTACCTCTGAACCTCATAGAC	2449
Db	2292	GTTATTTCTGCTCTTCCGAGTCTCGAGTGGGCTGCCCTGTACCTCTGAACCTCATAGAC	2351
QY	2450	CTCTAAGGGGAAAGGAGGAACAATTAGAGCGTGGCAATAGACTGGCAGGGCAGAGTACA	2509
Db	2352	CTCTAAGGGGAAAGGAGGAACAATTAGAGCGTGGCAATAGACTGGCAGGGCAGAGTACA	2411
QY	2510	AGCCAGAGACCCAGTGTCCAGCCCTTACCTGGGCTCTTACCCTGTGGCCAAACAGGGAGGGC	2569
Db	2412	AGCCAGAGACCCAGTGTCCAGCCCTTACCTGGGCTCTTACCCTGTGGCCAAACAGGGAGGGC	2471
QY	2570	TGATACCTCTTGTCTCTTCTTATGATGCCACTCTTAACATCTCAGCCCAACAATGCTCT	2629
Db	2472	TGATACCTCTTGTCTCTTCTTATGATGCCACTCTTAACATCTCAGCCCAACAATGCTCT	2531
QY	2630	CCACCCCTAGGGGGCTTGTGTCGATGGCAATPACTCAATTCGATTTGGAGGTTGGCCCTT	2689
Db	2532	CCACCCCTAGGGGGCTTGTGTCGATGGCAATPACTCAATTCGATTTGGAGGTTGGCCCTT	2591
QY	2690	TACAGGGGCAAGTATTTCTGTCTCAGTTCAACATGAATGAAGAGAGACTCCCTCTTTCTA	2749
Db	2592	TACAGGGGCAAGTATTTCTGTCTCAGTTCAACATGAATGAAGAGAGACTCCCTCTTTCTA	2651
QY	2750	CAGCTCACTTCTATCAGAGGCGCCAGGTGCTCAGAGCCAATTTGATGTTGCTTTCTGGG	2809
Db	2652	CAGCTCACTTCTATCAGAGGCGCCAGGTGCTCAGAGCCAATTTGATGTTGCTTTCTGGG	2711
QY	2810	ATGAGGAAGTAGGGTTAAACTCCCAAGTTTCTGTAG	2845
Db	2712	ATGAGGAAGTAGGGTTAAACTCCCAAGTTTCTGTAG	2747

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RESULT 10
US-10-117-723-19
; Sequence 19, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dimaenc, Radoje T.

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	TITLE OF INVENTION:	No. US2003029744A1el	Nucleic Acids and
	FILE REFERENCE:	Polypeptides	
	CURRENT FILING DATE:	2002-04-04	
	PRIOR APPLICATION NUMBER:	US/10/117,722	
	PRIOR FILING DATE:	2000-07-19	
	PRIOR APPLICATION NUMBER:	09/620,312	
	PRIOR FILING DATE:	2000-07-19	
	PRIOR APPLICATION NUMBER:	09/552,317	
	PRIOR FILING DATE:	2000-04-25	
	PRIOR APPLICATION NUMBER:	09/488,725	
	PRIOR FILING DATE:	2000-01-21	
	NUMBER OF SEQ ID NOS:	1104	
	SOFTWARE:	pl_fl_genes Version 1.0	
	SEQ ID NO 19		
	LENGTH:	2747	
	TYPE:	DNA	
	ORGANISM:	Homo sapiens	
	FEATURE:		
	NAME/KEY:	CDS	
	LOCATION:	(206)..(1618)	
	US-10-117-722-19		
	Query Match	83.1%; Score 2595.2;	DB 16; Length 2747;
	Best Local Similarity	96.6%; Pred. No. 0;	
	Matches 2700; Conservative	0; Mismatches	3; Indels 93; Gaps 1;
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QY	110	GAGGGAAATTGCGCGCGCGTCCCAGAGCCCTGCGCGCCCCGCTGAGCCGCATCACTT	169
Db	105	GAGGGAAATTGCGCGCGCGTCCCAGAGCCCTGCGCGCCCCGCTGAGCCGCATCACTT	164
QY	170	CCTCCCTGTGACCAACCGCGCTGCAAGTTAGAACCCTTGCAATSCCGTTTGGTGTGTA	229
Db	165	CCTCCCTGTGACCAACCGCGCTGCAAGTTAGAACCCTTGCAATSCCGTTTGGTGTGTA	224
QY	230	CTCTGGGCGACAAGAAACTATAACCAACCATTTGAGAGTGAATCTGACAGATATGATTTGG	289
Db	225	CTCTGGGCGACAAGAAACTATAACCAACCATTTGAGAGTGAATCTGACAGATATGATTTGG	284
QY	220	GACAGTCATCAAGATGAGAGATTTTGAAATCTTCCGSGCCAAGAACAGACAG	349
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Db	345	GCAAAGCTGCACACCTGCACAAAGATTCCAGAGCGGAGCGCCGACAAAGGTGCGAAAAGCTG	404
QY	410	CCAAAGACGAATAGGCACTCTCAAGATGTGGAAGCATCCCAACATCTTAACAGCTGTGG	469
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QY	470	ATGCTTTGTACCCCGCAAGAGATCTTATCTTCTGAGCTGACCAAGGGAGAGAG	529
Db	465	ATGCTTTGTACCCCGCAAGAGATCTTATCTTCTGAGCTGACCAAGGGAGAGAG	524
QY	530	TGTTTGACTGATCTCTGACCAAGGCTCTACTCTCGAGACGACACAAAGCAACGTGTAC	589
Db	525	TGTTTGACTGATCTCTGACCAAGGCTCTACTCTCGAGACGACACAAAGCAACGTGTAC	584
QY	590	GCGAAGTCTTGAGGCGCTGCTTATTTTGCACTCACTAAGATGTTGTCAGAGATTCCTCA	649
Db	585	GCGAAGTCTTGAGGCGCTGCTTATTTTGCACTCACTAAGATGTTGTCAGAGATTCCTCA	644
QY	650	AGCTGAGAACCTGGTTTTACTACAACCGGCTGGAAGACTCGAAGATTTGTCACTAGTACT	709
Db	645	AGCTGAGAACCTGGTTTTACTACAACCGGCTGGAAGACTCGAAGATTTGTCACTAGTACT	704
QY	710	TCCATCTGGCTAAGTAGAAATGCGCTCATCAAGAGCCCTGTGGAGCCCCGAGTATC	769
Db	705	TCCATCTGGCTAAGTAGAAATGCGCTCATCAAGAGCCCTGTGGAGCCCCGAGTATC	764

Db	1751	ATGCGCTGCTGCCCATGGCCCCCACAATCCAGTGGGCGATATACTAAGGAGTTCACGGGAGA	1810
QY	1868	GCACTCTCTGTTCTCTGTGTATATGTGTATAGTGGGACAGGCCAATGGCGAGGGCCGGC	1927
Db	1811	GCACTCTCTGTTCTCTGTGTATATGTGTATAGTGGGACAGGCCAATGGCGAGGGCCGGC	1870
QY	1928	CCGAGCCCTGTCATGGAATTCCCTGTGTGGCTTTTCTGTCTTTTGGCTTACCAATTTCT	1987
Db	1871	CCGAGCCCTGTCATGGAATTCCCTGTGTGGCTTTTCTGTCTTTTGGCTTACCAATTTCT	1930
QY	1988	GTTCCTTGTGGATGCTGCTCTAGGGATCTCAGGGGGCTCCTGCTCTCCTTCCCTTCC	2047
Db	1931	GTTCCTTGTGGATGCTGCTCTAGGGATCTCAGGGGGCTCCTGCTCTCCTTCCCTTCC	1990
QY	2048	CTTCTTGCTTCAACATTTCCCTTAGGCGAGGCCCTGCAAGTCCCAACTTCCAGGCCCTA	2107
Db	1991	CTTCTTGCTTCAACATTTCCCTTAGGCGAGGCCCTGCAAGTCCCAACTTCCAGGCCCTA	2050
QY	2108	AACTTGGGCGGCGCTTGCCCTAGAGACTGTGTCTCCAGGAGGGCCCTGTCAAGGTCCTAG	2167
Db	2051	AACTTGGGCGGCGCTTGCCCTAGAGACTGTGTCTCCAGGAGGGCCCTGTCAAGGTCCTAG	2110
QY	2168	GCTCCTGACATGAAAGTGTGTGCTGTGTGTGTGTGGCTCTCTTAGAGAGACATACAG	2227
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QY	2288	TAGGGAATCTGCTCACTAGCTGTGTGAAGTCTCTCAGAGTGGAGAGAAATGAATGAGAGGC	2347
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Db	2291	AGAANCT 2297	

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PRIORITY FILING DATE: 2000-11-14
PRIORITY APPLICATION NUMBER: US 10/003,650
PRIORITY FILING DATE: 2001-11-15
PRIORITY APPLICATION NUMBER: US 60/248,893
PRIORITY FILING DATE: 2000-11-15
PRIORITY APPLICATION NUMBER: US 09/797,039
PRIORITY FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: US 60/186,061
PRIORITY FILING DATE: 2000-02-29
PRIORITY APPLICATION NUMBER: US 10/217,168
PRIORITY FILING DATE: 2002-08-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 2297
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (154)...(1656)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2297)
OTHER INFORMATION: n = A,T,C or G
US-10-423-543-18

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Query Match	73.1%	Score 2383.4	DB 13	Length 2297
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2284	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

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RESULT 12
US-10-423-543-18
; Sequence 18, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, MiYoung
; APPLICANT: Williamson, Mark J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Bandaru, Rajasekhara
; TITLE OF INVENTION: NOVEL 219:0, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 22501, 17903, 3700, 21529, 26175, 26343, 56638,
; TITLE OF INVENTION: 18610, 33211, 21967, 41985, 41985, 38555
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-0230CNIM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325

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QY	308	AGAAGTTTGTGAAATCTTCCGGGCGAAGGACAAAGACACACAGGCAAGTCGACACTGCA	367
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QY	368	AGAAATTCCAAAGGGGAGCGCGCAAGTGGCGGAAAGCTGCCAAGACAGATAGGCA	427
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QY	548	ACCAAGGCTATCATCTCGAGCGAGACACAAAGCAAGTGTGTCGCGCAAGCTGTGAGGCGG	607
Db	491	ACCAAGGCTATCATCTCGAGCGAGACACAAAGCAAGTGTGTCGCGCAAGCTGTGAGGCGG	550
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Db	551	TGGCTATTGTGCATCTCACTCAAGATCGTGCAAGGAATCTCAAGCTGAGGAACCTGTTT	610
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PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/226,740
 PRIOR FILING DATE: 2000-08-21
 PRIOR APPLICATION NUMBER: US 09/861,801
 PRIOR FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: PCT/US01/16549
 PRIOR FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: US 60/205,508
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/801,267
 PRIOR FILING DATE: 2001-03-06
 PRIOR APPLICATION NUMBER: PCT/US01/07138
 PRIOR FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/187,454
 PRIOR FILING DATE: 2000-03-07
 PRIOR APPLICATION NUMBER: US 09/829,671
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: PCT/US01/40483
 PRIOR FILING DATE: 2001-04-11
 PRIOR APPLICATION NUMBER: US 60/197,508
 PRIOR FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/961,721
 PRIOR FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: PCT/US01/29904
 PRIOR FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: US 60/235,023
 PRIOR FILING DATE: 2000-09-25
 PRIOR APPLICATION NUMBER: US 10/045,367
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 60/246,561
 PRIOR FILING DATE: 2000-11-07
 PRIOR APPLICATION NUMBER: US 09/801,275
 PRIOR FILING DATE: 2001-03-06
 PRIOR APPLICATION NUMBER: PCT/US01/07074
 PRIOR FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: US 60/187,420
 PRIOR FILING DATE: 2000-03-07
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 SEQ ID NO: 1
 LENGTH: 2297
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 ORGANISM: Homo sapiens
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 NAME/KEY: CDS
 LOCATION: (154)..(1656)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(2297)
 OTHER INFORMATION: n = A,T,C or G
 US-10-170-789-1

Query Match 73.1%; Score 2283.4; DB 15; Length 2297;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2284; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 QY 248 ACTATTAACCAAGCCATCGAGGTGACTGACAGATGATTTGGAGCAAGTCAACAGACTG 307
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 QY 308 AGAGTTTGTGAATCTTCCGGGCGAAGACAAAGCAAGGCAAGTCAACCTTCA 367

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 QY 368 AGAAGTTCCAGAAACCGGAGCGCGCGAGAGTGGGAAAGCTGCCAAGACAGATAGGCA 427
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 QY 428 TCCTCAAGATGGTGAAGCATCCCAACATCTTACAGCTGTGTGATGTTTGTGACCCGCA 487
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Qy 2348 AGAAGCT 2354
Db 2291 AGAAGCT 2297

;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PT232
;; CURRENT APPLICATION NUMBER: US/09/764,868
;; PRIORITY FILING DATE: 2001-01-17
;; Prior application data removed - refer to PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 1510
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1378
;; LENGTH: 3915
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-764-868-1378

Query Match 60.1%; Score 1876.6; DB 9; Length 3915;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy 1931 AGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1990
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810 CTGAACCTGGCAATTAATCACTACCTGCAAGCC 776

RESULT 15
US-10-669-689-3
; Sequence 3, Application US/10669689
; Publication No. US20040038363A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000612DIV1
; CURRENT APPLICATION NUMBER: US/10/669,689
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7542
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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1211 CGGCTCAGACCCAGTGTGGCTCTAGCCACAGACTGCCACCCCGGGCTGAGGTGGG 1270
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1751 CAGAGAGTGGAGAGTGAAGGAGGCTTCTCACTGATCAATAGATCACTGGCATGATG 1810
4579 CAGAGAGTGGAGAGTGAAGGAGGCTTCTCACTGATCAATAGATCACTGGCATGATG 4638
1811 CCTGCGTCCCCCATGCCCCCAGTCCAGTCCAGTGGGGGATTAAGGGGTACCGGGAGAGCA 1870

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: April 23, 2004, 15:46:04 ; Search time 20 Seconds

(Without alignments)
2409.598 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581
Sequence: 1 MPFGCVTLGDKKKNYNQPSV.....SSKGEAGYAGQESGREAS 501

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1537.5	59.6	421	2	T30814 calmodulin-binding
3	797.5	30.9	374	1	SE0193 Ca2+/calmodulin-de
4	793	30.7	370	1	SE7347 Ca2+/calmodulin-de
5	713	27.6	348	2	T37321 Ca2+/calmodulin-de
6	645.5	25.0	310	2	B88640 protein K07A9.2 [i
7	620.5	24.0	474	1	TVR7C4 Ca2+/calmodulin-de
8	620.5	24.0	502	2	T52637 Ca2+/calmodulin-de
9	608	23.6	473	1	A53036 Ca2+/calmodulin-de
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11	552	21.4	542	1	A45025 Ca2+/calmodulin-de
12	551	21.3	542	1	A26464 Ca2+/calmodulin-de
13	545.5	21.1	589	2	SE6870 Ca2+/calmodulin-de
14	542	21.0	527	1	A31908 Ca2+/calmodulin-de
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16	534	20.7	478	1	A30355 Ca2+/calmodulin-de
17	529.5	20.5	414	2	JN0323 Ca2+/calmodulin-de
18	527.5	20.4	301	1	A40811 myosin-light-chain
19	521	20.2	335	2	T50290 calmodulin kinase
20	521	20.2	478	1	S04365 Ca2+/calmodulin-de
21	517.5	20.1	533	1	A34365 Ca2+/calmodulin-de
22	513.5	19.9	518	1	S43845 Ca2+/calmodulin-de
23	512.5	19.9	518	1	B4619 Ca2+/calmodulin-de
24	510.5	19.8	708	2	T33616 hypothetical prote
25	509.5	19.7	509	2	B44412 calmodulin-depende
26	509.5	19.7	530	2	D44412 Ca2+/calmodulin-de
27	502.5	19.5	516	1	JU0270 Ca2+/calmodulin-de
28	491.5	19.0	547	2	T3614 hypothetical prote
29	491.5	19.0	554	2	T05476 calcium-dependent

30	483.5	18.7	531	2	D85059 probable calcium d
31	483.5	18.7	1423	1	I37275 death-associated p
32	481.5	18.7	319	2	I38138 protein-serine kin
33	481.5	18.7	540	1	T01989 calcium-dependent
34	479.5	18.6	391	2	G87722 protein R06A10.4 [
35	473	18.3	532	2	T14335 protein kinase, ca
36	465	18.0	521	2	G96543 calcium-dependen
37	465	18.0	1176	2	JN0583 myosin-light-chain
38	463.5	18.0	1906	1	SE6835 myosin-light-chain
39	462.5	17.9	387	1	KTRB63 phosphotyrase kina
40	462	17.9	610	1	A49082 calcium-dependent
41	462	17.9	1147	2	A59307 myosin-light-chain
42	461.5	17.9	538	2	T08874 calcium-dependen
43	461	17.9	580	2	T40939 probable Ca-calmod
44	460.5	17.8	490	2	T08873 calcium-dependent
45	459.5	17.8	388	1	S00731 phosphorylase kina

ALIGNMENTS

RESULT 1

I56542
calmodulin-binding protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C/Accession: I56542
R/Godbout, M.; Brlander, M.G.; Hasel, K.W.; Danielson, P.E.; Wong, K.K.; Battenberg, E.L.
J. Neurosci. 14, 1-13, 1994
A/Title: IGS: a calmodulin-binding, vesicle-associated, protein kinase-like protein enric
A/Reference number: I56542; PMID:94110847; PMID:8283226
A/Accession: I56542
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-504 <RES>

A/Keywords: I56542; NTD:G349074; PIDN:AAA16633.1; PID:G349075
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C/Keywords: calmodulin binding
F/22-286/Domain: protein kinase homology <KIN>

Query Match 92.3%; Score 2383.5; DB 2; Length 504;
Best Local Similarity 91.9%; Pred. No. 36-94; 23; Indels 13; Gaps 2;
Matches 468; Conservative 5; Mismatches 23; Indels 13; Gaps 2;

QY	1	MPFGCVTLGDKKKNYNQPSVETDRYDLGVYKTEECETFRADKTTGKLATCKFOQRKDQ	60
DB	1	MPFGCVTLGDKKKNYNQPSVETDRYDLGVYKTEECETFRADKTTGKLATCKFOQRKDQ	60
QY	61	RKYRKAKEIGILKKVKNPILQLVDFVTRKEYFIFLELATGSEVPDWILDOGYSSR	120
DB	61	RKYRKAKEIGILKKVKNPILQLVDFVTRKEYFIFLELATGSEVPDWILDOGYSSR	120
QY	121	DRSNVROYLEAVAYHSLKIYRNKLKENVYRNKLKSKYVIDDFHLAKLNGLKEP	180
DB	121	DRSNVROYLEAVAYHSLKIYRNKLKENVYRNKLKSKYVIDDFHLAKLNGLKEP	180
QY	181	CGPEYLAPEVVGROGVRPVCMAIGVMTYLLSGNPFYEEVEDDYENHDKLFRKI	240
DB	181	CGPEYLAPEVVGROGVRPVCMAIGVMTYLLSGNPFYEEVEDDYENHDKLFRKI	240
QY	241	LAGDYEFDSPPYDDISQAAKDLVTRIMEVEDQRTTAEBASHEWISGNAASDKNIKGV	300
DB	241	LAGDYEFDSPPYDDISQAAKDLVTRIMEVEDQRTTAEBASHEWISGNAASDKNIKGV	300
QY	301	CAQIEKNPAPAKKKAQAVYTTLMKRLAPQSGSTAAGASATDPATPAPAGATPAAS	360
DB	301	CAQIEKNPAPAKKKAQAVYTTLMKRLAPQSGSTAAGASATDPATPAPAGATPAAS	360
QY	361	G-----ATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSATPATDGS	412
DB	361	G-----ATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSATPATDGS	412
QY	413	ATDGSVTPVTDRSATPATDGRATPATEESTVPTTOSAMLATKAAATPAPAAQDPSTAP	472
DB	413	ATDGSVTPVTDRSATPATDGRATPATEESTVPTTOSAMLATKAAATPAPAAQDPSTAP	472

DB 416 AHDGASTPTATDSATPATGRRATPATREBETVPAQAASSAPAKAAATPEFAVAQPDSTAL 475
 QY 473 EGATGQAPSSKGEAAGYAQESOREAS 501
 DB 476 EGATGQAPSSKGEAATGCAQESQREVS 504

RESULT 2

T30814
 Calmodulin-binding protein kinase - Fugu rubripes
 C/Species: Fugu rubripes
 C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 03-Jun-2002
 C/Accession: T30814
 R/Contact: A.J.; Clark, M.; Hawker, K.; Umanian, Y.; Wheller, D.; Bishop, M.; Elgar, G.
 FERS Lett. 443, 370-374, 1999
 A/Title: Three receptor genes for plasminogen related growth factors in the genome of th
 A/Reference number: Z20880; MUID:9914833; PMID:10025966
 A/Accession: T30814
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1421 <COT>
 A/Cross-references: EMBL:AF010348; NID:e1355080; PID:e1355083; PIDN:CAA09101.1
 C/denetic:
 A/Intons: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3

Query Match 59.6%; Score 1537.5; DB 2; Length 421;
 Best Local Similarity 76.2%; Pred. No. 1.5e-58;
 Matches 298; Conservative 36; Mismatches 42; Indels 15; Gaps 4;

QY 1 MPFGCVTLGDKKNYQSEVTDREYDQGVKTEPFCEIFRAKDKTGKLTCKKFGQRDG 60
 DB 1 MPFGCVTLGDKKNYQSEVTDREYDQGVKTEPFCEIFRAKDKTGKLTCKKFGQRDG 60
 QY 61 RKVRKAANEIGILKNVKNHNIQLVDFVTRKEVTFELATGREVFPMIIDQGYSSR 120
 DB 61 RKVRKAANEIMTLKVNKHNIQLVDFVTRKEVTFELATGREVFPMIIDQGYSSR 120
 QY 121 DTGNVVRQVLEAVAYVLSKTIHNRNKLLENLVYNNRKNKSYISPFHLAKLENGLIKPE 160
 DB 121 DTGNVVRQVLEAVAYVLSKTIHNRNKLLENLVYNNRKNKSYISPFHLAKLENGLIKPE 160
 QY 121 DTGNVVRQVLEAVAYVLSKTIHNRNKLLENLVYNNRKNKSYISPFHLAKLENGLIKPE 178
 DB 121 DTGNVVRQVLEAVAYVLSKTIHNRNKLLENLVYNNRKNKSYISPFHLAKLENGLIKPE 178
 QY 181 CGPEVYAPBVRGQRGRPVDCMAGVIMYIILSGNPPYEVEEDVDENHKNLFRKI 240
 DB 179 CGPEVYAPBVRGQRGRPVDCMAGVIMYIILSGNPPYEVEEDVDENHKNLFRKI 238
 QY 241 LAGDFEEDSYMDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 300
 DB 239 LAGDFEEDSYMDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 298
 QY 301 CAQIEKNPAPAKMKKAVRTTLMKRLPAPQSSST-AAAGASAT-DTAPGAAGATAA 358
 DB 299 CAQIEKNPAPAKMKKAVRTTLMKRLPAPQSSST-AAAGASAT-DTAPGAAGATAA 358
 QY 359 ASGATAPBEGDAAAASDNVAPADRSATPA 389
 DB 359 ASGATAPBEGDAAAASDNVAPADRSATPA 378

RESULT 3

S50193
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 N/Alternate names: CamKI
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S50193; A49682; A46038
 R/Contact: R.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
 Biochim. Biophys. Acta 1224, 156-160, 1994
 A/Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent pro
 A/Reference number: S50193; MUID:95035115; PMID:7948038
 A/Accession: S50193
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-374 <CHO>
 A/Cross-references: EMBL:L26288; NID:g439613; PIDN:AAA66944.1; PID:g439614
 R/Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.
 J. Biol. Chem. 268, 26512-26521, 1993
 A/Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification
 A/Reference number: A49682; MUID:9407534; PMID:8253780
 A/Accession: A49682

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HQP', 327, 'T', 329, 'TDS' <PIC>
 A/Cross-references: GB:L24907; NID:g406112; PIDN:AAA19670.1; PID:g406113
 R/Mochizuki, H.; Ito, T.; Hidaka, H.
 J. Biol. Chem. 268, 9143-9147, 1993
 A/Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase V
 A/Reference number: A46038; MUID:93232082; PMID:8386178
 A/Accession: A46038
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 12-36, 'T' <MOC>
 A/Experimental source: cerebrium
 A/Note: sequence extracted from NCBI backbone (NCBI:129927)
 C/Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
 C/Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
 F/18-276/Domain: protein kinase homology <KIN>
 F/26-34/Region: protein kinase ATP-binding motif
 F/293-299/Region: autoinhibitory
 F/302-314/Region: calmodulin binding
 F/177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 30.9%; Score 797.5; DB 1; Length 374;
 Best Local Similarity 41.9%; Pred. No. 2.5e-27;
 Matches 160; Conservative 73; Mismatches 128; Indels 21; Gaps 4;

QY 14 YNQSSEVTDRLDQGVKTEPFCEIFRAKDKTGKLTCKKFGQRDRKVRKAKNEIGI 73
 DB 14 YNQSSEVTDRLDQGVKTEPFCEIFRAKDKTGKLTCKKFGQRDRKVRKAKNEIGI 69
 QY 10 WKQAEIDIRDIYDFRDVGTGAFSEVILAEDEKRTQKVAICIAKAKALEGSEGNENIAV 69
 DB 10 WKQAEIDIRDIYDFRDVGTGAFSEVILAEDEKRTQKVAICIAKAKALEGSEGNENIAV 69
 QY 74 LKMTGHPNIIQLVDFVTRKEVTFELATGREVFPMIIDQGYSSRDTGNVVRQVLEAV 133
 DB 74 LKMTGHPNIIQLVDFVTRKEVTFELATGREVFPMIIDQGYSSRDTGNVVRQVLEAV 129
 QY 70 LHKTHPNTVMDIYESGHTYIMQVNSGGEFPDIVEKGFPTTERDASRLITQVLDVAV 129
 DB 70 LHKTHPNTVMDIYESGHTYIMQVNSGGEFPDIVEKGFPTTERDASRLITQVLDVAV 129
 QY 134 AYLSKTIHNRNKLLENLVYNNRKNKSYISPFHLAKLEN-GLIKEPGTPEYLAPEV 191
 DB 130 KYLHDLGIYHNDLKPENILYSLDEDSKIMSDGLKMEDEPGSLTAGCTPGYVAPEV 189
 QY 192 VGRQRYGPRVDCAIGVIMYIILSGNPPYEVEEDVDENHKNLFRKI 251
 DB 190 LAQKPYSKAVDQWSIGVAYIILGYPPEYDE-----NDATLFEQILKAEVEFPSPY 241
 QY 252 WDDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDGCAQIEKNPAPA 311
 DB 242 WDDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDGCAQIEKNPAPA 301
 QY 312 KWKKAVRTTLMKRLPAPQSSST-AAAGASAT-DTAPGAAGATAAASGATSAEGD 369
 DB 302 KWKKAVRTTLMKRLPAPQSSST-AAAGASAT-DTAPGAAGATAAASGATSAEGD 358
 QY 370 AARAKSDNVAPADRSATPATD 391
 DB 359 -----GSELPAPPPSSRAMD 374

RESULT 4

S57347
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
 N/Alternate names: CamKI
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S57347
 R/Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.;
 EMBO J. 14, 3679-3686, 1995
 A/Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struct

N/Alternate names: Ca2+/calmodulin-dependent protein kinase Gr

N/Contains: caldesmonin

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 11-Jun-1999

C/Accession: A41103; A41237; A32865; A41250; A32035; A60255; I53706

R/Onmede, C.A.; Bland, M.N.; Merrill, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991

A/Title: Relationship of gene encoding Ca(2+)/calmodulin-dependent protein kinase Gr at

A/Reference number: A41103; MUID:91288548; PMID:1648230

A/Accession: A41103

A/Molecule type: DNA

A/Residues: 47-141, 'NE', 144-474 <OH1>

A/Cross-references: GB:M74488; NID:G203219; PIDN:AAA40845.1; PID:G203220

A/Note: this sequence has been revised in reference A41237

A/Note: part of this sequence was confirmed by sequencing of cDNA to mRNA

R/Onmede, C.A.; Bland, M.N.; Merrill, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991

A/Reference number: A41237

A/Accession: A41237

A/Molecule type: DNA

A/Residues: 142-143 <OH2>

A/Cross-references: GB:M63334

A/Note: this is a revision to the sequence from reference A41103

R/Onmede, C.A.; Jensen, K.F.; Sahyoun, N.E.

J. Biol. Chem. 264, 5866-5875, 1989

A/Title: Ca(2+)/calmodulin-dependent protein kinase enriched in cerebellar granule cells

A/Reference number: A32865; MUID:89174647; PMID:2538431

A/Accession: A32865

A/Molecule type: mRNA

A/Residues: 250-474 <OH3>

A/Cross-references: GB:J04460; NID:G206172; PIDN:AAA1867.1; PID:G206173

R/Means, A.R.; Cruzalegui, F.; Lemagnere, B.; Needleman, D.S.; Slaughter, G.R.; Ono,

Mol. Cell. Biol. 11, 3960-3971, 1991

A/Title: A novel Ca(2+)/calmodulin-dependent protein kinase and a male germ cell-specific

A/Reference number: A41250; MUID:91304387; PMID:1649385

A/Accession: A41250

A/Molecule type: mRNA

A/Residues: 1-371, 'W', 373-408, 'Q', 410-474 <MEA>

A/Cross-references: GB:M64757

R/Ono, T.; Slaughter, G.R.; Cook, R.G.; Means, A.R.

J. Biol. Chem. 264, 2081-2087, 1989

A/Title: Molecular cloning sequence and distribution of rat caldesmonin, a high affinity

A/Reference number: A32035; MUID:89123272; PMID:2914893

A/Accession: A32035

A/Molecule type: mRNA

A/Residues: 306-371, 'M', 373-474 <ON1>

A/Cross-references: GB:J04446; NID:G203642; PIDN:AAA40990.1; PID:G203643

R/Ono, T.; Means, A.R.

Adv. Exp. Med. Biol. 255, 263-268, 1989

A/Title: Caldesmonin is a testis specific calmodulin-binding protein closely related to C

A/Reference number: A60255; MUID:90144189; PMID:2618865

A/Accession: A60255

A/Molecule type: protein

A/Residues: 335-363 <ON2>

A/Note: the amino end of caldesmonin was blocked

R/Bland, M.N.

Gene 137, 351-352, 1993

A/Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2+/C

A/Reference number: I53706; MUID:94131312; PMID:8299971

A/Accession: I53706

A/Status: preliminary; translated from GB/EMBL/DBDB

A/Molecule type: DNA

A/Residues: 1-37 <RES>

A/Cross-references: GB:J16699; NID:G310086; PIDN:AAA17443.1; PID:G310087

C/Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar granule

and in sperm cells.

C/Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology

C/Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/th

F/40-296/Domain: protein kinase homology <KIN>

F/48-57/Region: protein kinase ATP-binding motif

F/306-474/Product: caldesmonin #status predicted <GSP>

F/318-337/Region: calmodulin binding #status predicted

Query Match 24.0%; Score 620.5; DB 1; Length 474;
Best Local Similarity 39.0%; Pred. No. 9, 9e-20;
Matches 134; Conservative 70; Mismatches 127; Indels 13; Gaps 4;

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QY 38 IFRADKKTGKLTCKKFKQDRKRYKAAKNGIGLTKVKNPNTQLVDVFTREYFI 97
DB 56 VYRCKQKQTKPKYALKVTKVDKTI--VREIGVLRKSHPNITKKEIFETPEISL 112
QY 98 FLEIATGREGVDMILDOGYYSERDTSNVVRQVLEAVAYLSLTKIVHRNKLKENTLVYNNRL 157
DB 113 VLELVTTGSELFPDLIVRGYYSERDADAVKQILEAVAYLHENVIRHDLKPEVLLATPA 172
QY 158 KNSKIVISDFHLAKL--ENGLIKEPGTPEYLAPEVGRQYRYPVDCVAGIYMITLLS 215
DB 173 PDAPLKIDAFGLSKIVHQVLMKTVCGTPGCAPBEILRGCAYPEVDMMSVGIIITYILLC 232
QY 216 GNPFFYEVEEDYENHDKLFRKILAGDVEFDSFYWDIISQAKDLVTRLMVEEDQRI 275
DB 233 GFSEPFYD-----ERDQPFMRRIINCEYFFISPMWDEVSNAKDLVKKLIVLDPKKRL 285
QY 276 TAEBAISHWISGNAASDKNIKXGVCNOLKPNAPAKKKAIVRTIMKRLAPESOSTA 335
DB 286 TTFQOLHPVVTGKAAVFTVM-DTQCKKLOEFNAKKRLKAAVAVVASSRLSGASSSHNT 344
QY 336 AACGASATDTATPGAAAGATMAAASGATSAPEBDAPAAKSDNV 379
DB 345 IQESNKASSEAGPAQDGKDTPLENKKIQAGDHBAKAAADETM 388

```

RESULT 8
152637
Ca2+/calmodulin-dependent protein kinase IV beta polypeptide - rat
C/Species: Rattus sp. (rat)
C/Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 18-Jun-1999
R/Sakagami, H.; Kondo, H.
Brain Res. Mol. Brain Res. 19, 215-218, 1993
A/Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodul
A/Reference number: 152637; MUID:9401848; PMID:8412553
A/Accession: 152637
A/Status: preliminary; translated from GB/EMBL/DBDB
A/Molecule type: mRNA
A/Residues: 1-502 <RES>
A/Cross-references: GB:G65840; NID:G425383; PIDN:AA828372.1; PID:G425384
C/Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C/Keywords: ATP; calmodulin binding
F/68-324/Domain: protein kinase homology <KIN>
F/76-84/Region: protein kinase ATP-binding motif

Query Match 24.0%; Score 620.5; DB 2; Length 502;
Best Local Similarity 39.0%; Pred. No. 1e-19;
Matches 134; Conservative 70; Mismatches 127; Indels 13; Gaps 4;

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QY 38 IFRADKKTGKLTCKKFKQDRKRYKAAKNGIGLTKVKNPNTQLVDVFTREYFI 97
DB 84 VYRCKQKQTKPKYALKVTKVDKTI--VREIGVLRKSHPNITKKEIFETPEISL 140
QY 98 FLEIATGREGVDMILDOGYYSERDTSNVVRQVLEAVAYLSLTKIVHRNKLKENTLVYNNRL 157
DB 141 VLELVTTGSELFPDLIVRGYYSERDADAVKQILEAVAYLHENVIRHDLKPEVLLATPA 200
QY 158 KNSKIVISDFHLAKL--ENGLIKEPGTPEYLAPEVGRQYRYPVDCVAGIYMITLLS 215
DB 201 PDAPLKIDAFGLSKIVHQVLMKTVCGTPGCAPBEILRGCAYPEVDMMSVGIIITYILLC 260
QY 216 GNPFFYEVEEDYENHDKLFRKILAGDVEFDSFYWDIISQAKDLVTRLMVEEDQRI 275
DB 261 GFSEPFYD-----ERDQPFMRRIINCEYFFISPMWDEVSNAKDLVKKLIVLDPKKRL 313
QY 276 TAEBAISHWISGNAASDKNIKXGVCNOLKPNAPAKKKAIVRTIMKRLAPESOSTA 335
DB 314 TTFQOLHPVVTGKAAVFTVM-DTQCKKLOEFNAKKRLKAAVAVVASSRLSGASSSHNT 372

```

QY 336 AAGSASATDTATPGAGATPAAAGATSAPEGDAAPAAKSDNV 379
 Db 373 IQESNKASSSAQAPADGKXTDPLENMKGQGDHBAAPAADEMT 416

RESULT 9

A53036
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - human
 N:Alternate names: Ca2+/calmodulin-dependent protein kinase Gr; Cal-kinase IV
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: A53036; J02261; I53768
 R:Mosialos, G.; Hanislian, S.H.; Jawahar, S.; Vara, L.; Kieff, E.; Chatilla, T.A.
 J. Virol. 68, 1697-1705, 1994
 A:Title: A Ca(2+)/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed after tr
 A:Reference number: A53036; MUID:94149862; PMID:8107230
 A:Accession: A53036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-473 <MSO>
 A:Cross-references: GB:I24959; NID:g407005; PIDN:AAA18251.1; PID:g407006
 R:Kitani, T.; Okuno, S.; Fujisawa, H.
 J. Biochem. 115, 637-640, 1994
 A:Title: cDNA cloning and expression of human calmodulin-dependent protein kinase IV.
 A:Reference number: J02261; MUID:94375404; PMID:8089075
 A:Accession: J02261
 A:Molecule type: mRNA
 A:Residues: 1-473 <KIT>
 A:Cross-references: GB:I30742; NID:g487908; PIDN:BA06403.1; PID:g871845
 R:Blund, M.M.; Monroe, R.S.; Omstede, C.
 Gene 142, 191-197, 1994
 A:Title: The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protein
 A:Reference number: I53768; MUID:94252566; PMID:8194751
 A:Accession: I53768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-473 <RBS>
 A:Cross-references: GB:I17000; NID:g306478; PIDN:AAA3639.1; PID:g306479
 C:Comment: This protein is a Ca2+-responsive multifunctional protein kinase, which occur
 s system and in the immune system.
 C:Genetics:
 A:Gene: GDB:ILK
 A:Cross-references: GDB:6155815; OMIM:602366
 A:Map position: 11p15.5-11p15.4
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
 C:Keywords: ATP; calcium binding; calmodulin binding; phosphoprotein; phosphotransferase
 F:44-300/Domain: protein kinase homology <KIN>
 F:52-60/Region: protein kinase ATP-binding motif
 F:320-329/Region: calmodulin binding #status predicted
 F:8,12,15/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 23.6%; Score 608; DB 1; Length 473;
 Best Local Similarity 37.5%; Pred. No. 3.3e-19;
 Matches 141; Conservative 71; Mismatches 140; Indels 24; Gaps 6;

QY 38 IFRADKTTGKLTCKKFKQKGRKVRKAANKSIGILMKVGHPILOLVDFVTRKEYFI 97
 Db 60 VYRCQKQKQKRYALKVTKTVDKI---VREIIGVLRSLSHPIIKKKEIFETPTISL 116
 QY 98 FLEIATGAEVFWIIDOGYYSERDTSNVVRQVLEAVAYLHSIKYHRNLIKLENIYYNRL 157
 Db 117 VLEIATGSELFRIVYKESYSESDADAVKQILEAVAYLHENGIVHRDLKRENILYATPA 176
 QY 158 KNSKIVISDFHLAKL--ENGLIKERCCGPEYLAPEVGRQRVGRVDCMAIGVNYILLS 215
 Db 177 PDAPLKIAIDFGISKIVEHQVLMKTVCGTFGCAPBILRGCAVGEVDMWSGIIYYILLC 236
 QY 216 GNPPYEEVEEDYENHDKNLFRKILAGDYEFDSPYWMDISQAADIVYTRLMVEQDQRI 275
 Db 237 GFEPFYD-----ERGDQYFRRILNCEYFIFSPWMDVSLNAKDLYRKLIIVDPKKRL 289

Db 230 TTFQALQHPWVTGKAAKAEVH-DTAQKTLQEFNRRKILAAVKAIVVASSRLGSASSHGS 348
 QY 336 AAGSASATDTATPGAGATPAAAGATSAPEGDAAPAAK---SDVAPAPDR 384
 Db 349 IQESNKASSRSPSPIDGQEDMKALPEGEKIQGDGAQAQAELEMKVQALEKYGADI 408
 QY 385 SATPATDGSATPATDG 400
 Db 409 NAEBAPKVVPKXVEDG 424

RESULT 10

S17656
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S17656; A29878; I49571
 R:Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikelja, J.M.
 FEBS Lett. 289, 105-109, 1991
 A:Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-depende
 A:Reference number: S17656; MUID:91372388; PMID:1893997
 A:Accession: S17656
 A:Molecule type: mRNA
 A:Residues: 1-469 <JON>
 A:Cross-references: EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367
 R:Sikelja, J.M.; Hahn, W.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
 A:Title: Screening an expression library with a ligand probe: isolation and sequence of
 A:Reference number: A29878; MUID:87204263; PMID:3033675
 A:Accession: A29878
 A:Molecule type: mRNA
 A:Residues: 315-469 <SIK>
 A:Cross-references: GB:M16206; NID:g200360; PIDN:AAA39933.1; PID:g387512
 R:Sikelja, J.M.; Law, M.L.; Kao, F.
 Genomics 4, 21-27, 1989
 A:Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
 A:Reference number: I49571; MUID:89122027; PMID:2536634
 A:Accession: I49571
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 250-277; 'CPGI', 281-301, 'T', 303-338, 'X', 340-469 <RES>
 A:Cross-references: GB:J03057; NID:g192366; PIDN:AAA37366.1; PID:g192367
 A:Experimental source: brain
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
 C:Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/thr
 F:40-296/Domain: protein kinase homology <KIN>
 F:48-56/Region: protein kinase ATP-binding motif
 F:306-469/Product: calpermin #status predicted <CSP>
 F:318-337/Region: calmodulin binding #status predicted
 F:71/Active site: lys #status predicted

Query Match 23.3%; Score 602.5; DB 1; Length 469;
 Best Local Similarity 34.1%; Pred. No. 5.6e-19;
 Matches 151; Conservative 75; Mismatches 180; Indels 37; Gaps 10;

QY 38 IFRADKTTGKLTCKKFKQKGRKVRKAANKSIGILMKVGHPILOLVDFVTRKEYFI 97
 Db 56 VYRCQKQKQKRYALKVTKTVDKI---VREIIGVLRSLSHPIIKKKEIFETPTISL 112
 QY 98 FLEIATGAEVFWIIDOGYYSERDTSNVVRQVLEAVAYLHSIKYHRNLIKLENIYYNRL 157
 Db 113 VLEIATGSELFRIVYKESYSESDADAVKQILEAVAYLHENGIVHRDLKRENILYATPA 172
 QY 158 KNSKIVISDFHLAKL--ENGLIKERCCGPEYLAPEVGRQRVGRVDCMAIGVNYILLS 215
 Db 173 PDAPLKIAIDFGISKIVEHQVLMKTVCGTFGCAPBILRGCAVGEVDMWSGIIYYILLC 232
 QY 216 GNPPYEEVEEDYENHDKNLFRKILAGDYEFDSPYWMDISQAADIVYTRLMVEQDQRI 275
 Db 233 GFEPFYD-----ERGDQYFRRILNCEYFIFSPWMDVSLNAKDLYRKLIIVDPKKRL 285

Db 286 TTFQALQHPWVGKANKANFVEM-DTAKKLOQEFNARKKAAVAVASSRSGASSSTTS 344
Qy 336 AAQS--ASATDTATPGAGATATAAASGATSAPEGDAARA-AKSDNVA PADRSATPATDG 392
Db 345 IOENHKASDPPSTQDAKSTDLGKKQGEDEEDQVFAEASADBMKLO----- 395
Qy 393 SATPATDGSVTPATDGSITPATDGSVTPVTRSATPATDGRATPATTEESTVPTQSSAML 452
Db 396 SEVEEDAGVKEEETSSWVP--QDPEDELETDPEMKRDSSEKTKVEEEMPMTEBEA-- 452
Qy 453 ATKRAATPEPMAQP--DSTAPE 473
Db 453 -----PDAGGVPPQDAIOPE 468

RESULT 11

A45025
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999
C:Accession: A45025, S18915
R:Karis, U., Muller, U., Gilbert, D.J., Copeland, N.G., Jenkins, N.A., Harbers, K.
Mol. Cell. Biol. 12, 3644-3652, 1992
A:Title: Structure, expression, and chromosome location of the gene for the beta subunit
of a lethal mouse mutant.
A:Reference number: A45025, MUID:92334366; PMID:1321343
A:Accession: A45025
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-542 <KAR>
A:Cross-references: GB:X63615; GB:S40077; NID:G50275; PIDN:CAA45160.1; PID:G50276
A:Experimental source: BALB/c, brain
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:108750, NCBI:108751)
R:Karis, U., Muller, U., Gilbert, D.J., Copeland, N.G., Jenkins, N.A., Harbers, K.
submitted to the EMBL Data Library, December 1991
A:Reference number: S18915
A:Accession: S18915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-542 <KAR>
A:Cross-references: EMBL:X63615; NID:G50275; PIDN:CAA45160.1; PID:G50276
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
A:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 21.4%; Score 552; DB 1; Length 542;

Best Local Similarity 32.7%; Pred. No. 8, 9e-17;

Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

Qy 21 TDRYDGOVTKTEBFCIFRAKDKTG-----KLHTCKFKQKRGKRVKAAKNEIGILK 75

Db 11 TDEYQLVEDIGKAFSVVRKCVKLCGHEHYAAKINTKLSANDHQLEBEAR---ICR 66

Qy 76 MVKHPNLTQVDFVTRKEFYFLELATGHEVDMILDOGYSESDTSNVVRQVLEAVAY 135

Db 67 LKHSNIVRLHDSISEGFIYVFDVLTGGELEFDIVAREYSEADASHICQILLEVLAH 126

Qy 136 LHSIKIVRNKLENTLYYRNLRKSKIVISDFHLAKLENGILKE---PCGTPEYLAPEV 192

Db 127 CHQGVVHRDLKPEENLLASKCKGAAYKLDLFGIALTEVQDDQAMFGAGTPEYLSPEVL 186

Qy 193 GRQRYGPRVDCMAIGVIMYLLSGNPFVEVEEDVDENHDKLFFKILLAGVEFDSFVW 252

Db 187 RKEAYGKPVDMACGVILYLLNGVPEFWE-----DQH--KLTYQIKAGADFPSPEN 238
Qy 253 DDISAAKDLVTRLMEEVEDQRTAEBAISHEMI--SGNAADKNTKQGV-CAQIEKNFA 309
Db 239 DVTPEAKNLINQMLTINPAKRITTAHEALKHPVQCQSTVWAMHROETVEEC--LKFNFA 296
Qy 310 PAKKKAIVRTYLLMKLRAPESGSTAAQASATDTATPGAGATATAAASGATSAPEGD 369
Db 297 RRIKKGALITTMATATNFSVGRQTATPATWST-----AASGTTGLVEQKSLN-- 346
Qy 370 ABAKSDNVA PADRSATPATDGSATPATDGSVTPA-----TDGSITPATDGS 417
Db 347 ----KADGVKPTQNS--TKNSAITSPPKSLPPALAEQTTVINPVDG-IKESDSST 358
Qy 418 VTPVTRSATPATDGRATPATTEESTVPTQ 447
Db 399 NTIIEDEA-----KARKQEIITKTE 419

RESULT 12

A26464
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 11-Jun-1999
C:Accession: A26464
R:Bennett, M.K.; Kennedy, M.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1794-1798, 1987
A:Title: Deduced primary structure of the beta-subunit of brain type II Ca(2+)/calmodulin
A:Reference number: A26464; MUID:87175563; PMID:3470758
A:Accession: A26464
A:Molecule type: mRNA
A:Residues: 1-542 <BEN>
A:Cross-references: GB:M16112; NID:G206170; PIDN:AAA41866.1; PID:G206171
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
A:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 21.3%; Score 551; DB 1; Length 542;

Best Local Similarity 32.7%; Pred. No. 9, 8e-17;

Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

Qy 21 TDRYDGOVTKTEBFCIFRAKDKTG-----KLHTCKFKQKRGKRVKAAKNEIGILK 75

Db 11 TDEYQLVEDIGKAFSVVRKCVKLCGHEHYAAKINTKLSANDHQLEBEAR---ICR 66

Qy 76 MVKHPNLTQVDFVTRKEFYFLELATGHEVDMILDOGYSESDTSNVVRQVLEAVAY 135

Db 67 LKHSNIVRLHDSISEGFIYVFDVLTGGELEFDIVAREYSEADASHICQILLEVLAH 126

Qy 136 LHSIKIVRNKLENTLYYRNLRKSKIVISDFHLAKLENGILKE---PCGTPEYLAPEV 192

Db 127 CHQGVVHRDLKPEENLLASKCKGAAYKLDLFGIALTEVQDDQAMFGAGTPEYLSPEVL 186

Qy 193 GRQRYGPRVDCMAIGVIMYLLSGNPFVEVEEDVDENHDKLFFKILLAGVEFDSFVW 252

Db 187 RKEAYGKPVDMACGVILYLLNGVPEFWE-----DQH--KLTYQIKAGADFPSPEN 238

Qy 253 DDISAAKDLVTRLMEEVEDQRTAEBAISHEMI--SGNAADKNTKQGV-CAQIEKNFA 309

Db 239 DVTPEAKNLINQMLTINPAKRITTAHEALKHPVQCQSTVWAMHROETVEEC--LKFNFA 296

Qy 310 PAKKKAIVRTYLLMKLRAPESGSTAAQASATDTATPGAGATATAAASGATSAPEGD 369

Db 297 RRIKKGALITTMATATNFSVGRQTATPATWST-----AASGTTGLVEQKSLN-- 346

QY 370 AARAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDGSINPATDGS 417
 Db 347 ---KKADGVAFQTNSS---TKSSAITSFKGSLPALPOTVIRHPVDG-IKSSDST 398
 QY 418 VTPVTDRSATPATDGSATPATDGSVTPPTQ 447
 Db 399 NTTEDEDA-----KARKQELIKTTE 419

RESULT 13

568470
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Jun-1999
 C/Accession: S68470; 153501
 R/Urgidit, V.; Ashcroft, S.D.H.
 FEBS Lett. 358, 23-26, 1995
 A/Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent protein ki
 A/Reference number: 153501; MUID:95121451; PMID:7821422
 A/Accession: S68470
 A/Molecule type: mRNA
 A/Residues: 1-589 <UNQ>
 A/Cross-references: EMBL:X83375; NID:G603580; PIDN:CAA58289.1; PID:G603581
 A/Experimental source: pancreatic islets
 C/Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
 C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
 C/Keywords: alternative splicing; ATP; autophosphorylation; calmodulin binding; phospho
 F:12-272/Domain: protein kinase homology <KIN>
 F:20-28/Region: protein kinase ATP-binding motif
 F:287-311/Region: calmodulin binding #status predicted
 F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 21.1%; Score 545.5; DB 2; Length 589;
 Best Local Similarity 30.4%; Pred. No. 1.8e-16;
 Matches 143; Conservative 96; Mismatches 173; Indels 59; Gaps 13;
 QY 21 TDRYDLGVITKEEFCIFRAKDKTTG-----KLHTCKKFGQDRKRVKAKNEIGLK 75
 Db 11 TDEQLVIEDIGKAFSVRRVCYKCTGHEVYAKIINTKLSARHOKLERAR---ICR 66
 QY 76 MYKHPNITQLVDVFTVTRKEEYFLELATGREVFPMILDQGYSEBDSNVVRQVLEAVAY 135
 Db 67 LTKSNIIVLHDSISEEGFHYLVFDLVGGLFEDIVAREVYSEADASHCIGQLLEAVLH 126
 QY 136 LHSKLIYHNLKLENLVYVNRKSKIVISDFHLAKLENGLIKE---PGTPEYLAPEV 192
 Db 127 CHQGVVVRHDLKPEHLILASCKGAAVKLADFGLAIEVGQQAAMFGAGTGYLSPEVL 186
 QY 193 GROYGRVDCMAIGVIMYITLLSGNPFYEVEEDVDENHDKLFRKILGLDGYFSDPYW 252
 Db 187 RKEAYGKRVDTWACGVILYILVGVPPFWDE-----DQH--KLVOQIKGAADVFPSEW 238
 QY 253 DDISOAKDLVTRLMVEQDORITAEASISHEMI--SGNAASDKINIDGV-CAQIEKNFA 309
 Db 239 DTVPEAKNLINQMLTINPAKRIIHAELKHPWCQGSTVASMHRQETVEC--LKKFNA 296
 QY 310 RAKKKAVRVTTLMKRLAPBOS-----STAAQASATDTATPAGAGATPAA 358
 Db 297 RRLKGAITLTMLTRNFSAKSLKKAQGVKPTQNTKSSAI--TSPKSLPALLES 355
 QY 359 ASGATSAEGGAARAKSDNVAPADR--SATPATDGSATPATDGSVTPATDGSIT--TPA 413
 Db 356 SDSTVTTTEEDAKAPRISDILINSVRCGTPEAEGPSVAPPCCLPGLGIPPTSPSR 415
 QY 414 TDGSAVTPTDSATPATDGS-----RATPATBSTVPTQ 447
 Db 416 ISDILINSVRSGSTPEAEGLPVPGPPCPSPPTLPGLPFTPSRKQELIKTTE 466

C/Species: Rattus norvegicus (Norway rat)
 C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 11-Jun-1999
 C/Accession: A31908
 R/Tobimatsu, T.; Kameshita, I.; Fujisawa, H.
 J. Biol. Chem. 263, 16082-16086, 1988
 A/Title: Molecular cloning of the cDNA encoding the third polypeptide (gamma) of brain ce
 A/Reference number: A31908; MUID:89034067; PMID:2846534
 A/Accession: A31908
 A/Molecule type: mRNA
 A/Residues: 1-527 <TOC>
 A/Cross-references: GB:J04063; NID:G206151; PIDN:AAA1857.1; PID:G206152
 C/Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A/Note: acts on a variety of intracellular proteins; gamma and delta chains are expressed
 C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
 C/Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
 F:12-272/Domain: protein kinase homology <KIN>
 F:20-28/Region: protein kinase ATP-binding motif
 F:287-311/Region: calmodulin binding #status predicted
 F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 21.0%; Score 542; DB 1; Length 527;
 Best Local Similarity 34.4%; Pred. No. 2.3e-16;
 Matches 141; Conservative 77; Mismatches 146; Indels 46; Gaps 13;
 QY 21 TDRYDLGVITKEEFCIFRAKDKTT-----GKHTCKKFGQDRKRVKAKNEIGLK 75
 Db 11 TDQQLFEBLGKAFSVRRVCYKCTSTQRYAKIINTKLSARHOKLERAR---ICR 66
 QY 76 MYKHPNITQLVDVFTVTRKEEYFLELATGREVFPMILDQGYSEBDSNVVRQVLEAVAY 135
 Db 67 LKHPNIVLHDSISEEGFHYLVFDLVGGLFEDIVAREVYSEADASHCIGQLLESVNH 126
 QY 136 LHSKLIYHNLKLENLVYVNRKSKIVISDFHLAKLENGLIKE---CGTPEYLAPE 189
 Db 127 IHQHDIVHDLKPEHLILASCKGAAVKLADFGLAIEVGQQAAMFGAGTGYLSPE 183
 QY 190 EYVGRGRVPRVDCMAIGVIMYITLLSGNPFYEVEEDVDENHDKLFRKILAGDYPFS 249
 Db 184 EYLRKDPYKRPVDIYACGIIYILVGVPPFWDE-----DQH--KLVOQIAGAVIDFES 235
 QY 250 PWDIDISQAKDLVTRLMVEQDORITAEASISHEMI--SGNAASDKINIDGV-CAQIEK 306
 Db 236 FENDVITPEAKNLINQMLTINPAKRIIADQALKHRCVCRSTVASMHRQETVEC--LRK 293
 QY 307 NPAPAKKAVRVTTLMKRLAPBOSSTPAAQASATDTATPAGAGATPAAAGATSA 365
 Db 294 FNAARRLKALITLTVLVSNSFVGRQSSAPAPAS-----AAGLAGQAKSLKXK 345
 QY 366 PEGDAAPAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATD 415
 Db 346 SDGVYKRRKSSSVHLMPEQITVVAH-----ATDG-IKGSTSCNTTTE 389

RESULT 15

568470
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-E - human
 C/Species: Homo sapiens (man)
 C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 17-Mar-1999
 C/Accession: J05636
 C/Breen, M.A.; Ashcroft, S.J.H.
 Biochem. Biophys. Res. Commun. 236, 473-478, 1997
 A/Title: Human islets of Langerhans express multiple isoforms of calcium/calmodulin-deper
 A/Reference number: J05636; MUID:97382459; PMID:9240463
 A/Accession: J05636
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-556 <BRE>
 A/Cross-references: GB:U66063
 C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
 C/Keywords: phosphotransferase

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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:45:29 ; Search time 45 Seconds

(without alignments)
3512.769 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581 1 MFGCVTLGDKKXKNYQPSSEV.....SSKGEAAGYAQDSOREEAS 501

Sequence: 1 MFGCVTLGDKKXKNYQPSSEV.....SSKGEAAGYAQDSOREEAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MNC:*
8: SP_ORGANELLE:*
9: SP_PLANT:*
10: SP_TODENT:*
11: SP_VIRUS:*
12: SP_YEAST:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIA:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2577	99.8	501	4	Q8WTT8	Q8wtt8 homo sapien
2	2568	99.5	501	4	Q8WTC9	Q8wtc9 homo sapien
3	2563	99.3	501	4	Q8WCB2	Q8wcb2 homo sapien
4	2410.5	93.4	512	11	Q8WCD20	Q8wcd20 mus musculus
5	2403	93.1	473	4	Q8WH05	Q8wh05 homo sapien
6	2402.5	93.1	470	4	Q8WH85	Q8wh85 homo sapien
7	2398.5	92.9	470	4	Q8WBS8	Q8wbs8 homo sapien
8	2383.5	92.3	504	11	Q6S092	Q6s092 ratuus norv
9	2383.5	92.3	504	11	Q7SY49	Q7sy49 brachydantio
10	1602	62.1	333	4	Q8WNU4	Q8wnu4 homo sapien
11	1537.5	59.6	421	13	Q8WGM4	Q8wgm4 fuqu rubrip
12	786.5	30.5	395	13	Q8WYR3	Q8wyr3 xenopus lae
13	771	29.9	357	4	Q8WH13	Q8wh13 homo sapien
14	767.5	29.7	385	4	Q8WTH8	Q8wth8 homo sapien
15	767.5	29.7	385	11	Q8WY96	Q8wy96 mus musculus
16	764.5	29.6	367	11	Q8WWT7	Q8wwt7 mus musculus

17	762	29.5	378	13	Q8WTT8
18	761	29.5	382	13	Q8WTT8
19	757.5	29.3	377	11	Q8WTT8
20	749	29.0	476	11	Q8WTT8
21	748.5	29.0	405	5	Q8WTT8
22	747.5	29.0	481	4	Q8WTT8
23	746.5	28.9	476	4	Q8WTT8
24	746	28.9	460	4	Q8WTT8
25	743.5	28.8	477	11	Q8WTT8
26	731.5	28.3	337	13	Q8WTT8
27	731	28.3	299	11	Q8WTT8
28	720	27.9	309	11	Q8WTT8
29	716.5	27.8	342	11	Q8WTT8
30	716	27.7	377	11	Q8WTT8
31	715	27.7	343	11	Q8WTT8
32	715	27.7	343	11	Q8WTT8
33	715	27.7	348	5	Q8WTT8
34	715	27.7	355	11	Q8WTT8
35	713	27.6	348	5	Q8WTT8
36	705.5	27.3	324	5	Q8WTT8
37	660.5	25.6	284	5	Q8WTT8
38	659.5	25.6	284	5	Q8WTT8
39	620.5	23.4	502	11	Q8WTT8
40	604.5	23.4	469	11	Q8WTT8
41	589	22.8	385	13	Q8WTT8
42	578.5	22.4	716	4	Q8WTT8
43	577.5	22.4	424	11	Q8WTT8
44	575	22.3	755	11	Q8WTT8
45	563.5	21.8	695	4	Q8WTT8

ALIGNMENTS

RESULT 1
ID Q8WTT8 PRELIMINARY; PRT; 501 AA.
AC Q8WTT8;
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019256; AAH19256.1; -;
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; P:Protein kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; P:Protein kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 501 AA; 54353 MW; 1D6BFAADAD1D70 CRC64;

Query Match 99.8%; Score 2577; DB 4; Length 501;
Best Local Similarity 99.8%; Pred. No. 8.5e-147;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MFGCVTLGDKKXKNYQPSSEVTDYDGLGVTKTEEFCEIFRAKDKTKGLTKCKKPKKRG 60
1 MFGCVTLGDKKXKNYQPSSEVTDYDGLGVTKTEEFCEIFRAKDKTKGLTKCKKPKKRG 60

Query Match 99.3%; Score 2563; DB 4; Length 501;
 Best Local Similarity 99.6%; Pred. No. 5,9e-146;
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 DB 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 QY 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 DB 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 QY 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 DB 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 QY 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 DB 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 QY 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 DB 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 QY 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 360
 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 360
 DB 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 360
 QY 361 GATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 361 GATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 DB 361 GATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 480
 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 480
 DB 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 480
 QY 481 PSSKGEBAAGYAQESQREAS 501
 481 PSSKGEBAAGYAQESQREAS 501
 DB 481 PSSKGEBAAGYAQESQREAS 501

RESULT 4
 Q8VD20 PRELIMINARY; PRT; 512 AA.

AC Q8VD20
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to vesicle-associated calmodulin-binding protein.
 GN BC017634.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017634; AA017634.1; -.
 DR MGD; MGI:2384296; BC017634.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002290; Ser Thr_kinase.
 DR Pfam; PF00069; Pkinase; I.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; transferase.

SQ SEQUENCE 512 AA; 54819 MW; CFEFD4C43CC869A9 CRC64;
 Query Match 93.4%; Score 2410.5; DB 11; Length 512;
 Best Local Similarity 92.2%; Pred. No. 8.6e-137;
 Matches 474; Conservative 6; Mismatches 19; Indels 15; Gaps 2;

QY 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 DB 1 MPEGCVTLDGKKNNQPSSEVTDRIYDLGVITKEEFCIFRAKDKTTGKLATCKKFKQKRG 60
 QY 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 DB 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVDFWILDOGYSER 120
 QY 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 DB 121 DTSNVVRQVLEAVAYLHSLKIVHRNKLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
 QY 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 DB 181 CGTPEYLAPVEVGRQYGRPYDCAIGVIMYILISGNPPFEEVEEDDYENHDKLFRKI 240
 QY 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 DB 241 LAGDYEPDSFYWDISQAADLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
 QY 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 359
 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 358
 DB 301 CAQIEKNFAPAKMKKAVRTTLMKRLAPBEGSSTAASATDTATPGAAGATAAAS 358
 QY 360 -----SGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATD 407
 360 -----SGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATD 407
 DB 360 -----SGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSITPATD 407
 QY 408 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 467
 408 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 467
 DB 408 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 467
 QY 419 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 478
 419 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 478
 DB 419 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 478
 QY 468 DSTAPEGATGQAPSSKGEBAAGYAQESQREAS 501
 468 DSTAPEGATGQAPSSKGEBAAGYAQESQREAS 501
 DB 468 DSTAPEGATGQAPSSKGEBAAGYAQESQREAS 501
 QY 479 DSTALEGATGQAPSSKGEBAAGYAQESQREAS 512
 479 DSTALEGATGQAPSSKGEBAAGYAQESQREAS 512
 DB 479 DSTALEGATGQAPSSKGEBAAGYAQESQREAS 512

RESULT 5
 Q9H005 PRELIMINARY; PRT; 473 AA.

AC Q9H005
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZP564E0482.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=21154917; PubMed=11230166;
 RA Wieman S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.,
 RA Ansoerg W., Boecker M., Bloeker H., Bauersachs S., Blum N.,
 RA Lauber J., Duesterhoef A., Beyer A., Koehler K., Strack N.,
 RA Mews H.W., Ottenwaelder B., Obermaler B., Tange J., Heubner D.,
 RA Wambute R., Korn B., Klein W., Poustka A.;
 RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";
 RT Genome Res. 11:422-435 (2001).
 DR EMBL; AL136697; CAB66632.1; -.
 DR HSSP; O63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.

DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; P:kinase.
 DR Pfam: PF00069; kinase; 1.
 DR ProDom: PD000001; P:kinase; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 473 AA; 51208 MW; 8DFCE6C4F43262 CRC64;

Query Match 93.1%; Score 2403; DB 4; Length 473;
 Best Local Similarity 94.2%; Pred. No. 2.2e-136;
 Matches 472; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MPFGCVTLGDKKNYNOPSEVTDRIYDGOVKTBEFCEIFRAKDITGKLTCKKFKQRDG 60
 DB 1 MPFGCVTLGDKKNYNOPSEVTDRIYDGOVKTBEFCEIFRAKDITGKLTCKKFKQRDG 60
 QY 61 RRYRKAANEIGILKWKHPNIIQLVDVFTREKEYIFLELATGREVFDWILDQGYSER 120
 DB 61 RRYRKAANEIGILKWKHPNIIQLVDVFTREKEYIFLELATGREVFDWILDQGYSER 120
 QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 QY 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 DB 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 QY 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 DB 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 QY 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 DB 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 QY 301 CAQIEKNFAPAKWKAVRTTLMKRLAPESGSTAAQASATDTATPGAAGATPAAAS 360
 DB 273 CAQIEKNFAPAKWKAVRTTLMKRLAPESGSTAAQASATDTATPGAAGATPAAAS 332
 QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 DB 333 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 392
 QY 421 VTDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 480
 DB 393 ATDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 452
 QY 481 PSSKGEAAGYAQESQREAS 501
 DB 453 PSSKGEAAGYAQESQREAS 473

RESULT 6

Q8NC85 PRELIMINARY; PRT; 470 AA.

AC Q8NC85; DB 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ90418.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishi S., Kawai-Hito Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Nishimura Y.,
 RA "NEDO human cDNA sequencing project",
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK074899; BAC11278.1; -
 DR GO:0005524; F:ATP binding; IEA

DR GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO:0016740; F:transferase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR00719; P:kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; kinase; 1.
 DR ProDom: PD000001; P:kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 470 AA; 51686 MW; 16CC94CED91EB893 CRC64;

Query Match 93.1%; Score 2402.5; DB 4; Length 470;
 Best Local Similarity 93.6%; Pred. No. 2.3e-136;
 Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKNYNOPSEVTDRIYDGOVKTBEFCEIFRAKDITGKLTCKKFKQRDG 60
 DB 1 MPFGCVTLGDKKNYNOPSEVTDRIYDGOVKTBEFCEIFRAKDITGKLTCKKFKQRDG 60
 QY 61 RRYRKAANEIGILKWKHPNIIQLVDVFTREKEYIFLELATGREVFDWILDQGYSER 120
 DB 61 RRYRKAANEIGILKWKHPNIIQLVDVFTREKEYIFLELATGREVFDWILDQGYSER 120
 QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 61 RRYRKAANEIGILKWKHPNIIQLVDVFTREKEYIFLELATGREVFDWILDQGYSER 120
 QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 QY 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 DB 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 QY 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 DB 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 QY 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 DB 181 CGTPEYLAPEVVGQRGRVDCMAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
 QY 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 DB 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIAEASISHEWISGNAASDKNIKQGV 300
 QY 301 CAQIEKNFAPAKWKAVRTTLMKRLAPESGSTAAQASATDTATPGAAGATPAAAS 360
 DB 301 CAQIEKNFAPAKWKAVRTTLMKRLAPESGSTAAQASATDTATPGAAGATPAAAS 350
 QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 DB 351 -----AARSATPATDGSATPATDGSITPATDGSITPATDGSVTP 389
 QY 421 VTDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 480
 DB 390 ATDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 449
 QY 481 PSSKGEAAGYAQESQREAS 501
 DB 450 PSSKGEAAGYAQESQREAS 470

RESULT 7

Q8NB58 PRELIMINARY; PRT; 470 AA.

AC Q8NB58; DB 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ90813.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishi S., Kawai-Hito Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Body;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strusberg R.U., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Ranev U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Body;
 RA Strusberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055127; AAH5127.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 436 AA; 48704 MW; ECC8209E29483EE CRC64;

Query Match 63.3%; Score 1635; DB 13; Length 436;
 Best Local Similarity 65.2%; Pred. No. 2,5e-90;
 Matches 320; Conservative 52; Mismatches 63; Indels 56; Gaps 7;

QY 1 MFGCVTTGDKKNYNQPSFVTDYDLGVITKEPCEFFRAKDCTTGKLTCKKFKRKG 60
 DB 1 MFGCLKPEKDYNSPFEITDKYDLGVITKEPCEFFRAKDCTTGKLTCKKFKRKG 60
 QY 61 RYRRAAKKEIILKWKHFNILQVDVYETREKEYLFLLELATGREVDWILDOGYSER 120
 DB 61 RYRRAAKKEIILKWKHFNILQVDVYETREKEYLFLLELATGREVDWILDOGYSER 120
 QY 121 DTSNVROYLEAVAYLSKIVHRNKLLENLYYVNRKLNKSKIVISDFHLAKLENGLEP 180
 DB 121 DTSNVROYLEAVAYLSKIVHRNKLLENLYYVNRKLNKSKIVISDFHLAKLENGLEP 180
 QY 121 DTSNVROYLEAVAYLSKIVHRNKLLENLYYVNRKLNKSKIVISDFHLAKLENGLEP 180
 DB 121 DTSNVROYLEAVAYLSKIVHRNKLLENLYYVNRKLNKSKIVISDFHLAKLENGLEP 180
 QY 181 CGTPEYLADEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKI 240
 DB 181 CGTPEYLADEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKI 240
 QY 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGV 300
 DB 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGV 300
 QY 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGV 300
 DB 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGV 300
 QY 301 CAQIEKNFAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAAS 360
 DB 301 CAQIEKNFAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAAS 360
 QY 361 GATSAPEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
 DB 361 GATSAPEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
 QY 337 ---TAAAEAAASPE-----ADPAAGQETPQA-----ASEASTAPSS----- 373
 DB 337 ---TAAAEAAASPE-----ADPAAGQETPQA-----ASEASTAPSS----- 373
 QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEG-ATGQA 479
 DB 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEG-ATGQA 479

DB 374 -TAEISIASIE---VPAYE-----PAAAEASAAVOPPAEPVTVHVEPEQVPTSRONGEA 425
 QY 480 PESSKGEAAAG 490
 DB 426 PALDTVEQSG 436

RESULT 10
 OSNDU4 PRELIMINARY; PRT; 333 AA.
 ID OSNDU4;
 AC OSNDU4;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZ564G2082.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL83943; CAD38798.1; -.
 DR GO; GO:000524; F-ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00659; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS5011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS5011; PROTEIN KINASE DOM; 1.
 KM Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 333 AA; 34642 MW; 599E9307FF7D91E6 CRC64;

Query Match 62.1%; Score 1602; DB 4; Length 333;
 Best Local Similarity 99.1%; Pred. No. 1.7e-88;
 Matches 313; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 186 YLAPEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKIAGY 245
 DB 186 YLAPEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKIAGY 245
 QY 246 EFGSPYWDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGVCAQIE 305
 DB 246 EFGSPYWDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGVCAQIE 305
 QY 78 EFGSPYWDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGVCAQIE 137
 DB 78 EFGSPYWDISQAADLVTRIMEVEQDRIITAEPAISHWISGNAASDKNIXGVCAQIE 137
 QY 306 KNFARAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAASGATSA 365
 DB 306 KNFARAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAASGATSA 365
 QY 138 KNFARAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAASGATSA 197
 DB 138 KNFARAKMKKAVRTTLMKRLRAREQSTAAQASATDATTGAAGATAAASGATSA 197
 QY 366 PEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTPATDGS 425
 DB 366 PEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTPATDGS 425
 QY 198 PEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTPATDGS 257
 DB 198 PEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTPATDGS 257
 QY 426 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEGATGAPPSKG 485
 DB 426 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEGATGAPPSKG 485
 QY 258 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEGATGAPPSKG 317
 DB 258 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSTAPDEGATGAPPSKG 317
 QY 486 EEAAGYAEQREAS 501
 DB 318 EEAAGYAEQREAS 333

RESULT 11
 OSYGM4 PRELIMINARY; PRT; 421 AA.
 ID OSYGM4;
 AC OSYGM4;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)

01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Calmodulin binding protein kinase.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OC NCBI_Taxid=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9914833; PubMed=10025966;
 RA Cottage A.J., Clark W., Hawker K., Umransia Y., Wheller D., Bishop M.,
 RA Elgar G.;
 RT "three receptor genes for plasminogen related growth factors in the
 RT genome of the puffer fish Fugu rubripes.";
 RL FBS Lett. 443:370-374(1999).
 DR EMBL; AJ010348; CAA09101.1; -.
 DR PIR; T30814; T30814.
 DR HSP; Q63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR02290; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW SEQUENCE 421 AA; 47327 MW; 07C6A9FE44C96E4 CRC64;
 SQ
 Query Match 59.6%; Score 1537.5; DB 13; Length 421;
 Best Local Similarity 76.2%; Pred. No. 1,7e-84;
 Matches 298; Conservative 36; Mismatches 42; Indels 15; Gaps 4;
 QY 1 MPFGCTLGDKNNOSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDG 60
 DB 1 MPFGCTLGDKNNOSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDG 60
 QY 61 RKVKAANKNEIGLKMVGPNIQLVDFVTRKKEFFLELATGREVFDMILDQGYSSER 120
 DB 61 RKVKAANKNEIGLKMVGPNIQLVDFVTRKKEFFLELATGREVFDMILDQGYSSER 120
 QY 121 DTSNVVQVLEAVAYLHSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVQVLEAVAYLHSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 QY 121 DTSNVVQVLEAVAYLHSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVQVLEAVAYLHSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLENGLIKEP 180
 QY 181 CGTEPYLAPEVVGQRGRPRVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI 240
 DB 181 CGTEPYLAPEVVGQRGRPRVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI 240
 QY 179 CGTEPYLAPEVVGQRGRPRVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI 240
 DB 179 CGTEPYLAPEVVGQRGRPRVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI 240
 QY 241 LAGYEPDPSVWDIDISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDG 300
 DB 241 LAGYEPDPSVWDIDISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDG 300
 QY 239 LAGYEPDPSVWDIDISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDG 300
 DB 239 LAGYEPDPSVWDIDISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDG 300
 QY 301 CAQTEKPAKAKKAVVTTLMRLRLAPESQST-AAASQASAT-DATGGAAGATPAA 358
 DB 301 CAQTEKPAKAKKAVVTTLMRLRLAPESQST-AAASQASAT-DATGGAAGATPAA 358
 QY 299 CAQTEKPAKAKKAVVTTLMRLRLAPESQST-AAASQASAT-DATGGAAGATPAA 358
 DB 299 CAQTEKPAKAKKAVVTTLMRLRLAPESQST-AAASQASAT-DATGGAAGATPAA 358
 QY 359 ASGATSAPEGDAPAAKSDNVAPADRSATPA 369
 DB 359 ASGATSAPEGDAPAAKSDNVAPADRSATPA 369
 DB 359 -----SITKALSEKAAADQSTIPS 378

RESULT 12

Q8AYR3 PRELIMINARY; PRT; 395 AA.
 ID Q8AYR3
 AC Q8AYR3
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase.
 GN CAM-KI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saneyoshi T., Kume S., Mikoshiba K.;
 RT "calcium/calmodulin-dependent protein kinase.";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB082999; BAC19847.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS01008; PROTEIN_KINASE_ST; 1.
 KW kinase.
 KW SEQUENCE 395 AA; 43801 MW; 5381D04890B5D3AE CRC64;
 SQ
 Query Match 30.5%; Score 786.5; DB 13; Length 395;
 Best Local Similarity 39.9%; Pred. No. 1.9e-39;
 Matches 161; Conservative 85; Mismatches 131; Indels 27; Gaps 6;
 QY 16 QPSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDGKRYKAANKNEIGL 75
 DB 16 QPSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDGKRYKAANKNEIGL 75
 QY 16 QPSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDGKRYKAANKNEIGL 75
 DB 16 QPSEVTDRLDGOVTKTEFCEIFPAKDKTKGLTKCKKFKQKRDGKRYKAANKNEIGL 75
 QY 76 MYKHPNQLQVDFVTRKKEFFLELATGREVFDMILDQGYSSERDTSNVVQVLEAVAY 135
 DB 76 MYKHPNQLQVDFVTRKKEFFLELATGREVFDMILDQGYSSERDTSNVVQVLEAVAY 135
 QY 76 KIKHENVLAEDIVSPSHLYLMQVSGGELFDIVKGFYTERDASTLLRQVLDVAVSY 135
 DB 76 KIKHENVLAEDIVSPSHLYLMQVSGGELFDIVKGFYTERDASTLLRQVLDVAVSY 135
 QY 136 LSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLE-NGLIKEPCTEYLAPEVVG 193
 DB 136 LSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLE-NGLIKEPCTEYLAPEVVG 193
 QY 136 LSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLE-NGLIKEPCTEYLAPEVVG 193
 DB 136 LSLKIVHRLNKLBNLVYNNRLKNSKIYISDFHLAKLE-NGLIKEPCTEYLAPEVVG 193
 QY 194 RQYGRPVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 253
 DB 194 RQYGRPVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 253
 QY 196 QPYSKANDVCSIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 247
 DB 196 QPYSKANDVCSIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 247
 QY 254 DISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDGCAQTEKPAKAK 313
 DB 254 DISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDGCAQTEKPAKAK 313
 QY 248 DISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDGCAQTEKPAKAK 313
 DB 248 DISQAADLVTRLMVEVDORITAEASISHEWISGNAASDKNIKDGCAQTEKPAKAK 313
 QY 314 KXAVVTTLMRLRLAPESQSTAAASQASATDATTGGAAGATPAAASGATSAPEGDAPAA 373
 DB 314 KXAVVTTLMRLRLAPESQSTAAASQASATDATTGGAAGATPAAASGATSAPEGDAPAA 373
 QY 308 RQYGRPVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 253
 DB 308 RQYGRPVDCALIGVIMYILSGNPPFEVEEDDYENHDKLFRKI LAGYEPDPSVWD 253
 QY 374 AKSDNVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATPATDGS 417
 DB 374 AKSDNVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATPATDGS 417
 QY 353 CKSPS-NPYSFLSGVSSSSSAISAAGGDRP-RPSVITVTHAGS 394
 DB 353 CKSPS-NPYSFLSGVSSSSSAISAAGGDRP-RPSVITVTHAGS 394

RESULT 13

Q9HD31 PRELIMINARY; PRT; 357 AA.
 ID Q9HD31
 AC Q9HD31
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Camk1-like protein kinase.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT Verpoeijen S., Koenderman L., Coffey P.J.;
RA "Identification and characterization of CLK4: a novel granulocyte
RT G22/calmodulin-dependent kinase.";
RL Blood 010-8(2000).
CC 1.- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL, AF286366; AAC00534.1; -.
DR HESP, O63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004668; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot. kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot. kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding, kinase, Serine/threonine-protein kinase; Transferase
QO SEQUENCE 357 AA; 40189 MW; 1F814EEFA576FB4 CRC64;

Query Match	29.9%	Score 771	DB 4	Length 357
Best Local Similarity	40.3%	Pred. NO. 1.4e-38		
Matches 148, Conservative	84	Mismatches 109	Indels 26	Gaps 3

[illegible]

RESULT 14	
Q8IU85	
ID Q8IU85	PRELIMINARY; PRT; 385 AA

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to CamK1-like protein kinase (CaM-Kinase I like protein kinase
DE beta).
GN CKLIIK.BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ishitawa Y., Tokumitsu H., Inuzuka H., Murata-Hori M., Hosoya H.,
RA Kobayashi R.;
RT "Identification and characterization of novel components of
RT Ca²⁺/calmodulin-dependent protein kinase cascade.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RA Verplogsen S., Lammers U.L., Koedemans L.J., Coifer P.J.,
 RT "Identification and characterization of Cx1X, a novel granulocyte
 RT Ca++/calmodulin-dependent protein kinase.",
 RU Blood 0-0-0(2000).
 DR BMBL, BC035745, AAH35745.1, -
 DR BMBL, AB081726, BAC19846.1, -
 DR GO, GO:0005554, F:ATP binding, IEA.
 DR GO, GO:0004674, F:protein serine/threonine kinase activity, IEA.
 DR GO, GO:0004713, F:protein-tyrosine kinase activity, IEA.
 DR GO, GO:0006468, P:protein amino acid phosphorylation, IEA.
 DR InterPro, IPR000719, Prot_kinase.
 DR InterPro, IPR002390, Ser_thr_kinase.
 DR InterPro, IPR008271, Ser_thr_kinase.
 DR InterPro, IPR01245, Tyr_kinase.
 DR Pfam, PF00069, Pkinase, 1.
 DR ProDom, PD000001, Prot_kinase, 1.
 DR SMART, SMO0220, S_trc, 1.
 DR SMART, SMO0219, Tyrc, 1.
 DR PROSITE, PS00107, PROTEIN_KINASE_ATP, 1.
 DR PROSITE, PS0011, PROTEIN_KINASE_DOM, 1.
 DR PROSITE, PS0108, PROTEIN_KINASE_ST, 1.
 KW kinase.
 SQ SEQUENCE 385 AA; 42913 MW; 717467D019E30FC9 CRC64,

Query Match	29.7%	Score 767.5; DB 4	Length 385;
Best Local Similarity	40.4%;	Pred. No. 2.6e-38;	
Matches 152; Conservative	79;	Mismatches 122;	Indels 23; Gaps 57;

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QY      16 QPSEVTDRIYDGOVYIKTEFPOEIPFAUDKTKGKHTCKPKQRGRKRMAKNNEIGLX 75
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 QAEDIKKKFEFEEETIGTAFBSBVLAERKAQGKLFAYVCIPKKLKGHESISENIAVLAR 74
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      76 MYKHENIOLVDVEFTRKEYFIJELATGRREVFWILDOGYYSERDTSNNVROVLEAVAY 135
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75 KIKHENIVALIEDIYSPNHLLIVMOVGSGGLFDRIYVKGYTEDSABTLIRÖVLDANYY 134
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      136 IHSKIIVHRNTKLNLVYNNRLKNSKIVIISDPHLAKIE--NGLIKPECGTBYLAPEYVG 193
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      135 LHRMGIVHRDLKPENULLYYSQDEBSKIMSIDPGLSKMEKGQGVMSAQTGEYVAPEYLTA 194
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      194 RORYGRPYVDCAHIGVITNYITLLSGNPFFVEYEBEDYEHNDKLPFKILLAGDVFPFSFYWD 253
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      195 OKPYRKAVDCWMSGIVAYITLLCGPPFYDE-----NDSKLFEQIILKALEYFDSPLYWD 246
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      254 DTSOAKOLDVTLMVEODORITAEALSHEMIISGNASDNKINOGVOAQOIEKNFRAPAK 313
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      247 DISDBAKOFIRNLTMEKDYNKRTYCQAAHRPHIADDTLNNKNIHESVSAGIRKNTAKSKM 306
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      314 KZAAVYTILMKELR-----APEQSSTAQAQS---ASAIDTATPGA----ACGATAAAAS 360
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      307 ROAFPATNAVVRMRKLIHGSSLDSSNNAVSSSLASLOKDIAPETLCSFISSSGVSgv 366
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      361 GATSAPBEGDAABAAS 376
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      367 GAERRRPPTTVAVHS 382
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 15

Q8BW96 ID Q8BW96 PRELIMINARY; PRT; 385 AA.
AC Q8BW96;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CANK1-like protein kinase homolog.
GN E030025C1IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=2354683; PubMed=12466851;
RA The RIKEN Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK053173; BAC35285.1; -
DR MGD; MGI:2442190; E030025C1IRIK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_Thr_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
SQ SEQUENCE 385 AA; 42945 MW; 320EADCE057A1D55 CRC64;

Query Match 29.7%; Score 767.5; DB 11; Length 385;
Best Local Similarity 41.3%; Pred. No. 2.6e-38;
Matches 151; Conservative 77; Mismatches 115; Indels 23; Gaps 5;

QY 16 QPSEVTRDYDGVYKTEEFCEIFRANKTTGKLTCKKQKRDGRKVRKAANKNEIGILK 75
DB 15 QAEIDKRIEFKEKTLGTGAFSEVLAERKATGKLFVAVKCIPIKALKKESISENEIAYLR 74
QY 76 MVKPEPNIQLVDVYTRKEVFIFLELATGRVFPMDLQGYISRDTSNVVQVLEAVAY 135
DB 75 KIKENIYALDEDIYESPHMLYVMQVSGELFRIIVEKGYTEKDASTLIRQVLDVAVY 134
QY 136 LHSIKIVERNKLELVYVNRKSKIVISDFHLAKLE--NGLIKPCGTPPEYLAPVWG 193
DB 135 LHRKGIYARDLPENLLYISODESKIVISDFGLSKWEGKGDVWSTAGTIPGYAVEVLA 194
QY 194 RQRYGRPYCWAIGVIMYITLLSGNPPYEVEEDDYENHDKLPRKILAGDYEPDPSYWD 253
DB 195 QKPYSKAVDWSIGVIATILGYPPIYDE-----NDSKLFEGILKAYEFDSPYWD 246
QY 254 DISQAAKDLVTRLMEVEQDRTIAEBAISHWISGNAASDNINQDGVCAQIEKNPAPAKW 313
DB 247 DISDAKDFINLMKEDPNKRYTCQAAHPMIAGDTALSKNIHESVSAQIRKNFAFSKY 306
QY 314 KKAIVAVTLMLKLRAPF-----QSTAAQS---ASATDTATPGA---AGATAAAS 360
DB 307 ROAFNATVAVRMRLQGSNLDSSNAGVSSNLSAQDKCLAPSTLCSFLSSSSGVAGV 366
QY 361 GATSAAP 366
DB 367 GAERRP 372

Search completed: April 23, 2004, 15:49:42
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2004, 15:44:58 ; Search time 18 Seconds
(without alignment)

1449.286 Million cell updates/sec

Title: US-10-669-689-2
Perfect score: 2581
Sequence: 1 MFGCVTLGDKKNYQNPSEV.....SSKGEBAAGYAGDSQREKAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797.5	30.9	374	1 KCC1_RAT	Q63450 rattus norv
2	793.5	30.7	374	1 KCC1_MOUSE	Q91598 mus musculu
3	793	30.7	370	1 KCC1_HUMAN	Q14012 homo sapien
4	620.5	23.0	474	1 KCC4_RAT	P13234 rattus norv
5	608	23.6	473	1 KCC4_HUMAN	Q16566 homo sapien
6	602.5	23.3	469	1 KCC4_MOUSE	P08414 mus musculu
7	584.5	22.6	424	1 KPSH_HUMAN	P11801 homo sapien
8	564	21.9	740	1 DCK1_HUMAN	Q15075 homo sapien
9	563	21.8	664	1 KCCB_HUMAN	Q13554 homo sapien
10	559	21.7	756	1 DCK1_MOUSE	Q91198 mus musculu
11	558	21.6	433	1 DCK1_RAT	Q08875 rattus norv
12	552	21.4	542	1 KCCB_MOUSE	P28652 mus musculu
13	551	21.3	542	1 KCCB_RAT	P08413 rattus norv
14	542	21.0	527	1 KCCG_RAT	P11730 rattus norv
15	537	20.8	478	1 KCCA_HUMAN	Q09077 homo sapien
16	534	20.7	478	1 KCCA_RAT	P11275 rattus norv
17	530.5	20.6	295	1 KMLC_DICDI	P25333 dictyoscell
18	529.5	20.5	414	1 KCC1_EHEND	Q00771 emeryicella
19	525	20.3	438	1 KCCA_MOUSE	P11788 mus musculu
20	521	20.2	335	1 KCC1_SCHPO	Q9P712 schistosach
21	520.5	20.2	472	1 KCCG_HUMAN	Q13555 homo sapien
22	518	20.1	529	1 KCCG_MOUSE	Q02339 mus musculu
23	517.5	20.1	533	1 KCCD_RAT	P15791 rattus norv
24	507	19.6	382	1 KCC1_METAN	Q14408 metathizium
25	494.5	19.2	499	1 KCCD_HUMAN	P53355 homo sapien
26	494.5	19.2	1432	1 DAK1_HUMAN	P53355 homo sapien
27	487.5	18.9	370	1 DAK2_MOUSE	Q09473 mus musculu
28	486.5	18.8	1442	1 DAK1_MOUSE	Q09473 mus musculu
29	475.5	18.4	370	1 DAK2_HUMAN	Q09473 mus musculu
30	473	18.3	532	1 CDPK_DAUCA	P28512 daucus caro
31	467	18.1	386	1 KPSB_HUMAN	Q08824 bos taurus
32	465	18.0	1176	1 KML5_BOVIN	Q28824 bos taurus
33	463.5	18.0	1906	1 KML5_CHICK	P11799 gallus gall

ALIGNMENTS

34	462.5	17.9	386	1 KPSB_RABIT	P00518 oryctolagus
35	462	17.9	610	1 CDP1_ARATH	O06850 arabidopsis
36	462	17.9	1147	1 KML5_RABIT	P29294 oryctolagus
37	461	17.9	580	1 SRK1_SCHPO	O44547 schistosach
38	460	17.8	454	1 DAK3_HUMAN	O43293 homo sapien
39	459.5	17.8	387	1 KPSB_RAT	P13286 rattus norv
40	458	17.7	1914	1 KML5_HUMAN	O15746 homo sapien
41	457	17.7	387	1 KPSB_MOUSE	P07934 mus musculu
42	456.5	17.7	533	1 CDP2_ORYSA	P53683 oryza sativ
43	452.5	17.5	446	1 KCC1_YEAST	P27466 saccharomyc
44	450	17.4	448	1 DAK3_MOUSE	O54784 mus musculu
45	449	17.4	447	1 KCC2_YEAST	P22517 saccharomyc

RESULT 1
ID KCC1_RAT STANDARD; PRT; 374 AA.
AC Q63450; Q63084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=94075341; PubMed=8253780;
RA Picciotto M.R., Czernik A.O., Nairn A.C.;
RT "Calcium/calmodulin-dependent protein kinase I. cDNA cloning and
RT identification of autophosphorylation site.";
RT J. Biol. Chem. 268:26512-26521(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=lung;
RX MEDLINE=95035115; PubMed=7948038;
RA Cho F.S., Phillips K.S., Bogucki B., Weaver T.E.;
RT "Characterization of a rat cDNA clone encoding calcium/calmodulin-
RT dependent protein kinase I.";
RL Biochim. Biophys. Acta 1224:156-160(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF ISOFORM 2.
RC TISSUE=Brain;
RX MEDLINE=96182648; PubMed=8601311;
RA Goldberger J., Nairn A.C., Kuriyan J.;
RT "Structural basis for the autoinhibition of
RT calcium/calmodulin-dependent protein kinase I.";
RL Cell 84:875-887(1996).
CC -1- FUNCTION: Phosphorylates synapsin I.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
CC phosphorylated to be maximally active.
CC -1- SUBUNIT: Monomer.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=42 kDa;
CC IsoId=Q63450-1; Sequence=Displayed;
CC Name=2; Synonyms=37 kDa;
CC IsoId=Q63450-2; Sequence=VSP 004765;
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
CC subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

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CC entliequires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-ch).-----
CC
DR EMBL; L26907; AAA19670.1; -.
DR DR EMBL; L26288; AAA6944.1; -.
DR PIR; S50193; S50193.
DR PDB; 1A06; 08-APR-98.
DR PDB; IMKE; 07-JAN-03.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SMU0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KM Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.
FT DOMAIN 20 276
FT PROTEIN_KINASE.
FT NP_BIND 287 321 CALMODULIN-BINDING (BY SIMILARITY) .
FT BINDING 26 34 ATP (BY SIMILARITY) .
FT ACT_SITE 49 49 ATP (BY SIMILARITY) .
FT MOD_RES 141 141 BY SIMILARITY.
FT ACET_SITE 141 141 PHOSPHORYLATION (AUTO-) .
FT VARSP_LIC 177 177 TSQEGGGTASHGSLPTPGAGAACGCCRCDCVERGSELP
FT 323 PAPPSRRAM -> HQPGGTGRDS (in isoform 2) .
FT 374 /FTID=VSP_004765.
FT CONFLICT 112 112 F -> G (IN REF. 1) .
FT CONFLICT 118 118 A -> R (IN REF. 1) .
FT CONFLICT 309 309 A -> R (IN REF. 1) .
FT STRAND 11 12
FT HELIX 16 18
FT TURN 19 19
FT STRAND 20 25
FT STRAND 27 27
FT HELIX 29 33
FT STRAND 34 39
FT TURN 40 42
FT STRAND 45 52
FT STRAND 65 71
FT HELIX 72 72
FT TURN 76 77
FT STRAND 78 78
FT STRAND 81 86
FT STRAND 90 95
FT STRAND 102 102
FT HELIX 103 108
FT TURN 109 109
FT HELIX 115 134
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FT HELIX 144 146
FT STRAND 147 149
FT TURN 154 155
FT STRAND 158 160
FT TURN 183 184
FT HELIX 187 190
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FT TURN 197 197
FT HELIX 223 231
FT HELIX 223 233
FT TURN 232 233
FT HELIX 247 256
FT HELIX 261 263
FT HELIX 267 272
FT TURN 274 277
FT HELIX 287 297
FT TURN 302 304
FT STRAND 307 307
FT HELIX 309 315
SEQUENCE 374 AA; 41638 MW; 37898B3DEFO3JAB2 CRC64;
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Query Match	30.9%	Score 797.5	DB 1	Length 374
Best Local Similarity	41.9%	Prod. No. 6.5e-34		
Matches 160	Conservative 73	Mismatches 128	Indels 21	Gaps 4
QY	14	YNPSEVTEVDYDGOVYIKTEPECFEIPAKKTKGLTKCTCKCFQKRDGRKVRKAKNEIGI	73	
DB	10	WKQAEIDRDLDYPRDVLGTGAFSEVILAEKTRQKLVAKICAKKLLGEGSGENETIAV	69	
QY	74	LKNVKEPNLILQVDFVFTREKVEYIFIELATGSEVFWIIDOGYYSERDTSNVVRQVLEAV	133	
DB	70	LHKIKHPNIVALDVIYESGGHLYLMQVSGGELFRIVERKEGYETREDA SRLIFQVLDVAV	129	
QY	134	AYIHSLLKIYVRNKLKELVLYNRNLSKSVIISPHLAKLEN--GLIYEPGCTEYLAPEV	191	
DB	130	KYIHDIDGIYHRDKEPELFLYISDEDSCKIMISPGLSKMDPESVLTAGCTPDYVAPEV	189	
QY	192	VGRORGRPVDCMCAIGVYVITLLSGNPFVEEVEDDYENHDKNLPKTIAGDYEFPSPY	251	
DB	190	LAKPEYSKAVDCWSIGVIAITLLCGPPEFDE-----NDAKLPEQILLKAEYFSPY	241	
QY	252	WDIOSAKDLVTRLMVEVODQRITAEAISHWISGNAISDNKIKDGCACIENKFNARA	311	
DB	242	WDDISDSKADFIRHLMKEPKFTGCHLQHRINAGDTLMDKNINHSVEQIKKNRKS	301	
QY	312	KMKKAVRVTMLMKRLRAPE--QGSTAAAGSASATDTPAPGAGANTAAASGATSADEGD	369	
DB	302	KMKQAFNAATVAVHMRRLGLGTSQEGGCGYASHGELLTPAGBPAGACCCRDCEE---	358	
QY	370	AAPRASNVAPEADRSATPATD 391		
DB	359	-----GSELPPAPPESSRAMD 374		
RESULT 2				
KCCL_MOUSE				
ID	KCCL_MOUSE	STANDARD;	PRT;	374 AA.
AC	Q91Y58;			
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)			
DE	(CAM kinase I).			
GN	CAWK1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM R.P.			
FX	MEDLINE=22386257; PubMed=12477932;			
RA	Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Steinem C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hoskins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,			
RA	Ditichenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,			
RA	Rosa S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulik S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faley J., Heltón E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska J., Smalley D.E.,			
RA	Schmether A., Schein J.B., Jones S.U.M., Maira M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-I- FUNCTION: Phosphorylates synapsin I (By similarity).			
CC	-I- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.			

phosphorylated to be maximally active.

-1- SUBUNIT: Monomer (By similarity).

-1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK subfamily.

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EMBL; BC014825; AAH14825.1; -.

MED; MG1:1098535; CamK1.

GO; GO:0006913; P:nucleocytoplasmic transport; IDA.

GO; GO:0007165; P:signal transduction; IDA.

InterPro; IPR000719; Prot_Kinase.

InterPro; IPR008271; Ser_thr_pkin_AS.

InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Transferrase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding.

FT DOMAIN 20 276 CALMODULIN-BINDING (BY SIMILARITY).

FT NP_BIND 26 34 ATP (BY SIMILARITY).

FT BINDING 49 49 ATP (BY SIMILARITY).

FT ACT_SITE 141 141 BY SIMILARITY.

FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT SOURCE 374 AA; 41624 MW; 37889CDAY17D3AB2 CRC64; (BY SIMILARITY).

SO SEQUENCE

Query Match 30.7%; Score 793.5; DB 1; Length 374;

Best Local Similarity 41.6%; Pred. No. 1e-33;

Matches 159; Conservative 73; Mismatches 129; Indels 21; Gaps 4;

14 YNPSEVTDYVDIGOVYKTEEFCEIPFAKDTGKLTCKKFGKRGKVRKAKNEIGI 73

10 WKQAEIDRDYDPRDVGTCGAFSEVILAEKRTOKVATKICAKKALBEGEGMEINAV 69

74 LKRVKHEINILQVDFVTRKVEFIFELATGREVFMIIDOGYSESDTGNVVRQYLEAV 133

70 LHKIKENIYALDIDYSSGHLVIMQVSGELFRIVKGYTERDASRLIFQYLDLV 129

134 AYHSKIVIRNKLKENVLVYNNLKSIVISDFHLAKLN--GLIKPGCTEYLAPEV 191

130 KYLHDLGIIVHRDKPENLILYISDEDSKIMISDFGLSKMEDPSSVSTACGTGYVAPV 189

192 VGSQRYRPPVCAALGVIMYIILSGNPFVEYEDDYENHDKLPRKILAGYREDSRY 251

190 LAQPPYSKAVDCWSIGVIAIYLICGPPFYDE-----NDAKLFEQILKAYEYDSEP 241

252 WDISCAKOLVTRLMVEVODORTAEASHEWISGNAADKNIKDGVCAQIEKPFAPA 311

242 WDISDSADKQFIRKLKPEKRTCGQLCHFMIGADTLDKNIHQSVSEQIKNFAAS 301

312 KMKKAVVVTIMKRLRAPE--QSSFAAAGASATDTTPGACGATAAAAGATSAPEGD 369

302 KMKQAFNAIVAVRMRLKLGTSQEGGQSGTSGHELLTTPAGSPAPAGCCCRDCCVP 358

370 AARAKSDNVAPADRSATPATD 391

359 -----GSELPFAPPPSSRAMD 374

RESULT 3

KCQ1 HUMAN STANDARD; PRT; 370 AA.

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase type I (PC 2.7.1.123) (CAM kinase I).

GN CAMK1.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RM [1]

RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-49.

RX MEDLINE=95369239; PubMed=7641687;

RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D., Edelman A.M., Snyderman R., Means A.R.;

RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain structure and activation by phosphorylation at threonine-177 by calcium-calmodulin dependent protein kinase I kinase.";

RL EMBL J. 14:3679-3686(1995).

RL [2]

RP SEQUENCE OF 1-9.

RC TISSUE=Platelet;

RX MEDLINE=12665801; PubMed=12665801;

RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A., Thomas G.R., Vandeckerkhove J.;

RT "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides.";

RL Nat. Biotechnol. 21:566-569(2003).

CC -1- FUNCTION: Phosphorylates synapsin I.

CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.

CC -1- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be phosphorylated to be maximally active.

CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Ubiquitous.

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK subfamily.

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EMBL; L41816; AAA9458.1; -.

PIR; S57347; S57347.

HSSP; Q63450; 1A06.

DR Genew; HGNC:1459; CAMK1.

DR MIM; 604998; -.

DR GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. . .; TAS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

DR Transferrase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding.

FT DOMAIN 20 276 PROTEIN KINASE.

FT NP_BIND 26 34 CALMODULIN-BINDING (BY SIMILARITY).

FT BINDING 49 49 ATP (BY SIMILARITY).

FT ACT_SITE 141 141 BY SIMILARITY.

FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-).

FT FT K->R; LOSS OF ACTIVITY.

FT WTGENSE 370 AA; 41337 MW; 57FA20EC800FA76C CRC64;

Query Match: 30.7%; Score 793; DB 1; Length 370;
Best Local Similarity 43.7%; Pred. No. 1.1e-33;
Matches 156; Conservative 69; Mismatches 120; Gaps 3

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QY 14 YNPSSEVTRDYLQGVITKEEFCEIFRAKDTTKGTLTKCKFKQGRKVRKAANKNEIGI 73
Db 10 WKQAEEDIRIVYFRVLTGTAFSVILAEADRQTQVAKIACIKAEKLEGGSGMEVEIAY 69
QY 74 LKNVKEPNITLQVDVFTREKVEYFIFLELATGREVFDWILDGGYSESDTSNVVQVLEAV 133
Db 70 LHKIKRPNITVALDDIYESGGLYLIMQVSGCELFSDIIVEGFTYERDASRLIFQYLDAY 129
QY 134 AYIHSIKYIRKULKEENLYYTRKLNKSKIYSDPHAKLEN--GLIPEPGTFEYLAPEV 191
Db 130 KYIAMDGIYHRDLKRENLLYYSLDSDSKIMSDGLSRMEDPGSVLSTACPGFYAPEV 189
QY 192 VGRGRGRVVDCAIVGVIYITLISGNPFYEVEVEDDYENHDKULFKILAGYEPDSY 251
Db 190 LMQKPYSKAVDCMSIGVATYILCGYPPFYDE-----NDAKLFEQILKAIEYFDSY 241
QY 252 WDIOISAAADLYTRLMVEYEQDQRIITAEFAISHWYISGNAASDKNIKGVCAQIEKRFAPA 311
Db 242 WDIISASADFLRHLMEKDEPERFCEQALQHPHIAQDTALDNIHQSVEQIKKIFAS 301
QY 312 KMKAVRVITLMKRLAPR--QSGTMAQSAATDTATPGAAGATATTAASGATSAP 366
Db 302 KMKQAVNATAVVAVRHVKRLQLGHSQCGQQTASHGELLTPVAGVPAAGCCRCDCVER 358

RESULT 4
AC KCQA RAT STANDARD; PRT; 474 AA.
AC KCQA RAT
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
GN (EC 2.7.1.123) (Cam kinase-GR) (CamK IV) (Calpermin).
GN CMK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RX [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RP MEDLINE=91288548; PubMed=1648230;
RA Olmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RT kinase Gr and calpermin: a gene within a gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=91304387; PubMed=1649355;
RA Means A.R., Cruzalegui F., Lemsguerrese B., Needleman D.S.,
RA Slaughter G.R., Ono T.;
RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT cell-specific calmodulin-binding protein are derived from the same
RT gene.";
RL Mol. Cell. Biol. 11:3960-3971(1991).
RN [3]
RN SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=89174647; PubMed=2538431;
RA Olmstede C.-A., Jensen K.F., Sahyoun N.;
RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT granule cells. Identification of a novel neuronal
RT calmodulin-dependent protein kinase.";
RL J. Biol. Chem. 264:5866-5875(1989).
RN [4]
RP STRAIN=Sprague-Dawley;
RX MEDLINE=89123272; PubMed=2914893;
RN [5]
RP STRAIN=Sprague-Dawley;
RX MEDLINE=89123272; PubMed=2914893;
```

RT "Molecular cloning sequence and distribution of rat caldesmon, a
high affinity calmodulin-binding protein.";
J. Biol. Chem. 264:2081-2087(1989).
[5]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96094352; PubMed=7493991;
RA Sun Z., Means R.L., LeMagueresse B., Means A.R.;
RT "Organization and analysis of the complete rat calmodulin-dependent
protein kinase IV gene.";
J. Biol. Chem. 270:29507-29514(1995).
CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE.
CC -1- FUNCTION: IN CEREBELLAR GRANULE CELLS.
CC -1- FUNCTION: CALDESMON IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=2 isoforms, 1 and 2/Testis-specific, are produced by use
CC of alternative promoters;
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ due to the use of alternative promoters
CC and alternative splicing;
CC Name=1; Synonyms=Calcium-calmodulin-dependent protein kinase type
CC IV catalytic chain
CC IsoId=P1334-1; Sequence=displayed;
CC Name=2; Synonyms=Calspermin;
CC IsoId=P1334-2; Sequence=VSP_004789;
CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
CC is testis specific.
CC -1- PTM: The N-terminus of calspermin is blocked.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Camk
CC subfamily.
CC
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CC
CC -----
DR EMBL; M63334; AAA40865.1; -;
DR EMBL; M74488; AAA40845.1; ALT_SEQ.
DR EMBL; M64757; AAA40856.1; -;
DR EMBL; M64757; AAA40857.1; -;
DR EMBL; J04600; AAA41867.1; -;
DR EMBL; J04446; AAA40590.1; -;
DR PIR; A41103; TVRTCA.
DR HSSB; O63450; IAO6.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Prodom; PD000001; Prot kinase; 1.
DR SMART; SMO02230; S_TKC_1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP_1.
DR PROSITE; PS00108; PROTEIN KINASE_ST_1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM_1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Testis; Alternative splicing;
KW Alternative promoter usage.
KW DOMAIN 42 296 PROTEIN KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 POLY-GLU.
FT VARSPLIC 1 305 Missing (In isoform 2).
FT CONFLICT 372 372 I -> M (IN REF. 2 AND 4).
FT SEQUENCE 474 AA; 5313 MW; 56F71AC5644DED23 CRC64;


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Db 396 SEVENKAGVVEERTSSNV--QDPDELLETDDPKMKRSESKLVSVEEMDPMTBEA-- 452
Oy 453 ATKAALPEPMAQP--DSTAPE 473
Db 453 -----PDAGLGVPQDQALQPE 468

RESULT 7
KFSH HUMAN
AC P11801; Q9NY19; STANDARD; PRT; 424 AA.
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase H1 (BC 2.7.1.37) (PSK-H1).
GN PSKH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RX MEDLINE=20541713; PubMed=11087665;
RA Brede G., Solheim J., Troen G., Prydz H.,
RT "Characterization of PSKH1, a novel human protein serine kinase with
RL centrosomal, Golgi, and nuclear localization.",
RN Genomics 70:82-92(2000).
RP [2]
RP SEQUENCE OF 199-348 FROM N.A.
RA MEDLINE=87092414; PubMed=22948189;
RX Hanks S.K.;
RT "Homology probing: identification of cDNA clones encoding members of
RT the protein-serine kinase family.",
RL Proc. Natl. Acad. Sci. U.S.A. 84:388-392(1987).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: Activity depends on Ca(2+) concentration.
CC -1- SUBCELLULAR LOCATION: Localized in the nucleolus A-sensitve Golgi
CC compartment, at centrosomes, in the nucleus with a somewhat
CC speckle-like presence, and more diffusely in the cytoplasm.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues and cell lines
CC tested with the highest level of abundance in testis.
CC -1- PTM: Autophosphorylated on serine residues.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -----
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CC -----
DR EMBL; AJ272212; CAB91984.1; -.
DR EMBL; M14504; AA36519.1; -.
DR PIR; B26368; B26368.
DR HSSP; Q63450; 1A06.
DR GENE; HGNC:9529; PSKH1.
DR MIM; 177015; -.
DR GO; GO:0005524; F:ATP binding; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0006466; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00063; PKinase; 1.
DR ProDom; PDO00001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Trasnlaase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Golgi stack; Nuclear protein.

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FT	DOMAIN	98	355		PROTEIN KINASE.
FT	NR BIND	104	112		ATP (BY SIMILARITY).
FT	BINDING	127	127		ATP (BY SIMILARITY).
FT	ACT SITE	218	218		BY SIMILARITY.
FT	MOD RES	360	380		PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD RES	381	381		PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ	SEQUENCE	424 AA;	48035 MM;	B35775J7DDC1238BD CRC64;	
 Query Match 22.6% Score 584.5; DB 1; Length 424; Best Local Similarity 39.5%; Pred. No. 4.5e-23; Matches 132; Conservative 67; Mismatches 98; Indels 37; Gaps 8					
DQ	20	VMDRYDVGIVITEBFECEIFPAKDKTKGKLTCKFKQ--RDGRKYRAAKNEIGILKNV	77		
DQ	94	VIAKDIDIKLRIGSGFSFNVAVEHARROPALMIETKKREGEV---CESLARVLRRV	150		
DQ	78	KAPNTLIQLVDVEVTREKEVFIELELATGREVFWILDGGYSEEDTSNVRQVLEAVAYIH	137		
DQ	151	RANITIIQLVEVEFETGERVYMVMELATGSELFDRIIAGKSPTERDAIRVLQMVDGVRIHL	210		
DQ	138	SLKIYHRNKULENLVYTRKLNSKTIVSDPHLA---KLENGLIKPCCGPEPLAEVNG	193		
DQ	211	ALGITHTRLDKPENLIYYHFGDSKIIITDFGLSARKKGDDCLMKTYGTGPETIAEVLV	270		
DQ	194	RDRGPGVDMALGIYMTITLSGNPPFYEEVEDDYENHNKLFRLKLAGDYEFDSPYND	253		
DQ	271	RKPYNYSVMMALGIYAILISGMFPF---EDD--NTRLRYQTLLRKYSYSGSPNP	322		
DQ	254	DISOAAKDLVTLMVEODORTTAEASISHEMISGNAASD--KNIXDGYCAQIEKNPAPA	311		
DQ	323	SVSNAKDEIDBLLVDPGAMTMLQLRLRHVVVMAASSMKNLH---RSISQN----	374		
DQ	312	KMKKAVRTTLMKRILRAPEGSGTAAPSASATDT	345		
DQ	375	-----LLKRASSRCQSQTSAQSYRSSRST	398		
 RESULT 8 DCK1_HUMAN STANDARD; PRT; 740 AA. ID DCK1_HUMAN O15075; DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 42, Last annotation update) DI 10-OCT-2003 (Rel. 42, Last annotation update) DE Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1). GN DCAMKL1 OR KIA0369. OS Homo sapiens (Human). OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. OX NCBI_TaxId=9606; RN [1] RP SEQUENCE FROM N.A. (ISOFORM 1). RC TISSUE=Brain; RX MEDLINE=97349984; PubMed=9205841; RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; RL DNA Res. 4:i:141-150(1997). [2] RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). RC TISSUE=Fetal brain; RX MEDLINE=99156863; PubMed=10036192; RA Soresey-Alaoui K., Srivastava A.K.; RT "DCAMKL1, a brain-specific transmembrane protein on 13q12.3 that is similar to doublecortin (DCX)." ; RL Genomics 56:121-126(1999). [3] RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4). RX MEDLINE=98419166; PubMed=9747029; RA Omori Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y.,					

RA Takahashi E.-I., Fujiwara T.;
 RT "Expression and chromosomal localization of KIAA0369, a putative
 RT kinase structurally related to Doublecortin.",
 RL J. Hum. Genet. 43:169-177(1998).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=99162404; PubMed=10051403;
 RA Matsumoto N., Pilz D.T., Ledbetter D.H.;
 RT "Genomic structure, chromosomal mapping, and expression pattern of
 RT human DCAMKL1 (KIAA0369), a homologue of DCX (Klfs).",
 RL Genomics 56:179-183(1999).
 CC -1- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
 CC SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
 CC BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
 CC SYSTEM.
 CC -1- ALTERNATIVE PRODUCTS.
 CC Event=Alternative splicing; Named Isoforms=4;
 CC Comment=Additional isoforms seem to exist. Type A (AS and AL)
 CC and type B (BS and BL) isoforms differ respectively by the
 CC presence or absence of the doublecortin domain. An alternative
 CC splicing occurring in 3' of the mRNA produces the long (L)
 CC instead of the short (S) isoforms;
 CC Name=2; Synonyms=AL;
 CC IsoId=O15075-1; Sequence=Displayed;
 CC Name=1; Synonyms=AS;
 CC IsoId=O15075-2; Sequence=VSP_004907;
 CC Name=3; Synonyms=BS;
 CC IsoId=O15075-3; Sequence=VSP_004905, VSP_004906, VSP_004907;
 CC Name=4; Synonyms=BL;
 CC IsoId=O15075-4; Sequence=VSP_004905, VSP_004906;
 CC -1- TISSUE SPECIFICITY: IN FETAL TISSUES, HIGHLY EXPRESSED IN BRAIN,
 CC DETECTABLE IN LUNG AND LIVER, BUT NOT IN KIDNEY. IN ADULT TISSUES,
 CC EXPRESSED UBICITOUSLY IN THE BRAIN, DETECTABLE IN THE HEART,
 CC LIVER, SPLEEN, THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE
 CC AND COLON. THE TYPE A ISOFORMS SEEM TO BE EXPRESSED PREDOMINANTLY
 CC IN FETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN
 CC BOTH FETAL AND ADULT BRAIN.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
 CC subfamily.
 CC -1- SIMILARITY: Contains 2 doublecortin domains.
 CC -----
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 CC -----
 DR EMBL: AB002367; BAA20824.1; --
 DR HSSP: Q63450; 1A06.
 DR GeneW: HGNC:2700; DCAMKL1.
 DR MIM: 604742; --
 DR GO: GO:0005897; C:integral to plasma membrane; TAS.
 DR GO: GO:0004672; F:protein kinase activity; TAS.
 DR GO: GO:0005057; F:receptor signaling protein activity; TAS.
 DR GO: GO:0007417; P:central nervous system development; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR003533; DCX.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_Thr_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF03607; DCX; 2.
 DR Pfam: PF00069; PKinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00537; DCX; 2.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS50309; DC; 2.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE_CT; 1.
 DR Transfaser; Serine/threonine-protein kinase; ATP-binding; Repeat;
 KW Neogenesis; Alternative splicing.

FT	DOMAIN	57	143	DOUBLECORTIN 1.
FT	DOMAIN	186	269	DOUBLECORTIN 2.
FT	DOMAIN	288	340	SER/PRO-RICH.
FT	DOMAIN	390	647	PROTEIN KINASE.
FT	NP BIND	396	404	ATP (BY SIMILARITY).
FT	BINDING	419	419	ATP (BY SIMILARITY).
FT	ACT SITE	511	511	BY SIMILARITY.
FT	DOMAIN	698	701	POLY-ARG.
FT	VARSP-LIC	1	307	Missing (in isoform 3 and isoform 4).
FT	VARSP-LIC	308	313	/FTid=VSP_004905.
FT	VARSP-LIC	308	313	PASTS -> MLEIE (in isoform 3 and isoform 4).
FT	VARSP-LIC	687	740	/FTid=VSP_004906.
FT	VARSP-LIC	687	740	TTALDKERQVFRFRNRQDVRSRYKAQAPAPINSESEDYSP
FT	VARSP-LIC	687	740	SSSETVSPNSP -> LDHGFTKSGSLDYQCGMYWI
FT	VARSP-LIC	687	740	RPPLIRGRFSEDEPATRM (in isoform 1 and isoform 3).
FT	VARSP-LIC	687	740	/FTid=VSP_004907.
FT	VARSP-LIC	687	740	SEQUENCE 740 AA; 82223 MW; D7B6D855099A315C CRC64;
FT	VARSP-LIC	687	740	Query Match 21.9%; Score 564; DB 1; Length 740;
FT	VARSP-LIC	687	740	Best Local Similarity 35.6%; Pred. No. 9.2e-22;
FT	VARSP-LIC	687	740	Matches 119; Conservative 65; Mismatches 126; Indels 24; Gaps 4;
QY	11	KKNVNPSEVTDRDYDGVYKTEEPCEIPRAKDRTGKLTCKKFGKRDGRKVRKAARNE	70	
DB	377	EEGFOIPATTEHYKXGRITGDGNFAVKECVSRNAREYALKIKKCKRGHEHIONE	436	
QY	71	IGILNKVKNBNILQLVDPVTRKREYFLELATGREVFMIDQGYSERDTSNVTRQVL	130	
DB	437	VSLIRKRNBNVILLEMDVPTELVLVMEVKGDLFPAISTNKYTRDASGMLYNLA	496	
QY	131	EAVAYLHSLKIVRNKLNLVYVNRKNSK-LIVSDFFLAKLNLKEPCGTPETVLA	189	
DB	497	SAIKYHLSINIVARDIKPNLVLVEHQDSKSLKLDGFLGATIVDPLVTVGTPPYVAP	556	
QY	190	EAVGRGRYGRPVDCMAIGVIMYLLSGNPPYEEVEDENYHDKVLFRKILAGDYEPFS	249	
DB	557	ELIAETGYGLKVDIMAGVITTYLLCGFPFF-RSGGDQD---VLPQILMGQVDFPS	610	
QY	250	PYWDISQAAKDLVTRLMVEYODORTTAEASISHEWISGNAASDKNIKGVCAQIEKNPA	309	
DB	611	PYWDNVDSKAKELITMLLVVDVQRFSAVQVLEHPVNDGLPENHQLSVAGKIKKHN	670	
QY	310	RAIKKRAVRVTITMKLRAPESGTAASASAT	343	
DB	671	-----TGPKNSTAGVSIAT	687	

RESULT 9
 KCCB_HUMAN STANDARD; PRT; 664 AA.
 AC Q13554; Q95437; Q95438; Q95599; Q9UGH7; Q9UGH8; Q9UGH9; Q9UNX0;
 AC Q9UNY0; Q9UP00; Q9Y5M4; Q9Y5P4;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II beta chain
 DE (EC 2.7.1.123) (Cam-kinase II beta chain) (Cam kinase II beta subunit)
 DE (CamK-II beta subunit).
 GN CAMK2B OR CAMKB OR CMK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCB1_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 5, 6 AND 7).
 RC TISSUE=Brain;
 RX MEDLINE=20317016; PubMed=10858498;
 RT Wang P., Wu Y., Zhou T.H., Sun Y., Pei G.;
 RT "Identification of alternative splicing variants of the beta subunit
 RT of human Ca(2+)/calmodulin-dependent protein kinase II with different
 RT activities";

RL FB55 Lett. 475:107-110(2000).
 RP [2]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Skeletal muscle;
 RA Leddy J.J., Sallih M., Tuana B.S.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 5).
 RC TISSUE=Brain;
 RA Li G.Y., Cooper N.G.F.;
 RT "Molecular cloning and sequencing of human calcium/calmodulin
 RT dependent protein kinase II beta subunit."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RP [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 5).
 RC TISSUE=Insulinoma;
 RX MEDLINE=22386257; PubMed=10819240;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Rochlitz H., Voigt A., Lankat-Buttgerieit B., Goke B., Heimberg H.,
 RA Nauck M.A., Schlemann U., Schatz H., Pfeiffer A.F.;
 RT "Cloning and quantitative determination of the human
 RT Ca2+/calmodulin-dependent protein kinase II (CaMK II) isoforms in
 RT human beta cells."
 RL Diabetologia 43:465-473 (2000).
 RP [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lung;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Pirange C.,
 RA Rana S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schermer A., Schein J.E., Jones S.J.W., Mastra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [6]
 RP SEQUENCE OF 302-603 FROM N.A. (ISOFORM 2).
 RX MEDLINE=97214619; PubMed=9060999;
 RA Tombes R.M., Krystal G.W.;
 RT "Identification of novel human tumor cell-specific CaMK-II variants."
 RL Biochem. Biophys. Acta 1355:281-292 (1997).
 CC -1- FUNCTION: CaM-kinase II (CaMK2) is a prominent kinase in the
 CC central nervous system that may function in long-term potentiation
 CC and neurotransmitter release.
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ENZYME REGULATION: Autophosphorylation of CaMK2 plays an important
 CC role in the regulation of the kinase activity.
 CC -1- SUBUNIT: CaMK2 is composed of four different chains: alpha, beta,
 CC gamma, and delta. The different isoforms assemble into homo- or
 CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Comment=The variable region of the CaMK2B protein is encoded by
 CC at least 7 exons (V1 to V7). Alternative splicing within this
 CC region gives rise to CaMK2B isoforms;
 CC Name=4;
 CC IsoId=Q13554-1; Sequence=Displayed;
 CC Name=1; Synonyms=Beta;
 CC IsoId=Q13554-2; Sequence=VSP_004776;
 CC Name=2; Synonyms=Beta1, Beta'E;
 CC IsoId=Q13554-3; Sequence=VSP_004770, VSP_004771, VSP_004775,

CC CC
 CC Name=3; Synonyms=Beta2;
 CC IsoId=Q13554-4; Sequence=VSP_004770, VSP_004771, VSP_004774,
 CC VSP_004776;
 CC CC
 CC Name=5; Synonyms=Beta4, BetaB;
 CC IsoId=Q13554-5; Sequence=VSP_004770, VSP_004771, VSP_004776;
 CC Name=6; Synonyms=Beta6;
 CC IsoId=Q13554-6; Sequence=VSP_004773, VSP_004776, VSP_004777;
 CC Name=7; Synonyms=Beta7;
 CC IsoId=Q13554-7; Sequence=VSP_004772, VSP_004776;
 CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in adult and fetal
 CC brain. Expression slightly lower in fetal brain.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL, AF078803; AAD42035.1; -
 CC EMBL, AF081572; AAD42036.1; -
 CC EMBL, AF083419; AAD42038.1; -
 CC EMBL, AF081924; AAD42037.1; -
 CC EMBL, AF140350; AAD42070.1; -
 CC EMBL, U23460; AAC99802.1; -
 CC EMBL, AF112472; AAD03744.1; -
 CC EMBL, AF112471; AAD03743.1; -
 CC EMBL, AJ252236; CAB65120.1; -
 CC EMBL, AJ252237; CAB65121.1; -
 CC EMBL, AJ252238; CAB65122.1; -
 CC EMBL, BC019070; AAH19070.1; -
 CC EMBL, U50358; AAB16663.1; -
 CC Genew, HGNC:1461; CaMK2B.
 CC MIM, 607707; -
 CC GO, GO:0004685; P:calcium/calmodulin-dependent protein kinase. . . TAS.
 CC GO, GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC GO, GO:0007165; P:signal transduction; TAS.
 CC InterPro, IPR000719; Prot_kinase.
 CC InterPro, IPR008271; Ser_Thr_kin_AS.
 CC Pfam, PF00069; pkinase; 1.
 CC ProDom, PD000001; Prot_kinase; 1.
 CC PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE, PS00108; PROTEIN_KINASE_GT; 1.
 CC PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
 CC Phosphorylation; ATP-binding; Neuron; Alternative splicing.
 CC DOMAIN 14 272
 CC NP BIND 20 28
 CC BINDING 43 43
 CC ACT_SITE 136 136
 CC DOMAIN 291 301
 CC VARSPLIC 316 316
 CC FT FT
 CC VARSPLIC 317 340
 CC FT FT
 CC VARSPLIC 316 408
 CC FT FT
 CC VARSPLIC 354 377
 CC FT FT
 CC VARSPLIC 354 392
 CC FT FT
 CC VARSPLIC 379 393
 CC FT FT
 CC VARSPLIC 410 531
 CC FT FT
 CC VARSPLIC 557 582
 CC FT FT
 CC Missing (in isoform 2, isoform 3 and
 CC isoform 5).
 CC /FTId=VSP_004771.
 CC /FTId=VSP_004771.
 CC /FTId=VSP_004772.
 CC /FTId=VSP_004773.
 CC /FTId=VSP_004773.
 CC /FTId=VSP_004774.
 CC /FTId=VSP_004775.
 CC /FTId=VSP_004775.
 CC Missing (in isoform 1, isoform 2, isoform
 CC 3, isoform 5, isoform 6 and isoform 7).
 CC /FTId=VSP_004776.
 CC Missing (in isoform 6).


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FT FT CONFLICT 68 68 /FTID=VSP 004777.
FT FT CONFLICT 533 533 L -> V (IN REF. 3).
SQ SEQUENCE 664 AA; 72726 MW; 9E8C82918D986614 CRC64;

Query Match 21.8%; Score 563; DB 1; Length 664;
Best Local Similarity 31.0%; Pred. No. 9.2e-22;
Matches 157; Conservative 86; Mismatches 181; Indels 80; Gaps 15;

QY 21 TDRYDGLQVYKTEEFCEIFRAADKTTG-----KLTCKKQQRDRGRYKKAANEIGLK 75
DB 11 TDEYQLYEDIGKCAFVSVRVCVLTGHEVAAKIINTKLSARDHQLEAREAR-----ICR 66
QY 76 MYGHPILDLVDFVYRKYEFIFLELATGREFVDMILDOGYSEEDTSNVNVCYLENAVY 135
DB 67 LKHGSHVHLHDSISEEGHYVLFVDTLVTGELFEDVAEYSEADASHCIQIILEAVLH 126
QY 136 LHSLEKIVHNLKLENIYVYNRNLKNSKIVISDFHLAKLENGLIKE---PGCTPEYLAPRY 192
DB 127 CHOMGVTHHDLPENILLASKCKGAAYKLADFGLAIEVGDDQAFGFRAGTGYLSPEYL 186
QY 193 GQRYGRPYDCWAGIYIMYTLISGNPFYEVEEDDYENHDKLPRLIAGDYEDSEPYW 252
DB 187 RKEAYGKPYDIWACGYITLILVGYPPFYDE-----DQH--KLVOQIKAGAYDPSPPEW 238
QY 253 DDISAAKDLVTRLMVEVODQRTAEALISEHWI--SGNAASDKNIKQGV-CAQIEKNFA 309
DB 239 DVTPEAKKLIQMLINPAKRITAEALHFMVOCRSVASMGRHOETVEC--LKKENA 296
QY 310 RAKMKKAVVITLTKRLAPBQSTAAQASATDTATGAGAGATAAASGATSAPSGD 369
DB 297 RKKLKALITTLATNFSVGRQTTPATMST-----AASGTWGLVEQAKLNLN-- 346
QY 370 AARAAKSDNVAPADSSATPATDGSATPATDGSATPA-----TDGSIPTATDGS 417
DB 347 ----KKADEVKQNTS---TKNSAATSPKGTLPRALEPQTVVHNPDG-IKSSSDSA 398
QY 418 VTPVTDRSATPATDGRATPATBESIVPTTQSSAMLATKAATPEPAMAQPOSTAEGA-- 475
DB 399 NTTIEDEDA-----KAPRVDPILSSVRSGSRSGARSGAPACSPAPFSLPAPS 446
QY 476 -----TGQAPSSKGEBAAG 490
DB 447 PRISDILNSVRSGSTPEAEGLSAG 472

RESULT 10
DCK1_MOUSE STANDARD; PRT; 756 AA.
ID DCK1_MOUSE
AC Q9JLM8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase DCKM1 (EC 2.7.1.1-) (Doublecortin-
DE like and CAM kinase-like 1).
GN DCKM1 OR DCLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20004649; PubMed=10533048;
RA Burgess H.A., Martinez S., Reiner O.,
RT "Kila0369, doublecortin-like kinase, is expressed during brain
RT development."
RL J. Neurosci. Res. 58:567-575(1999).
CC -1- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
CC SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
CC BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
CC SYSTEM (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Camk

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CC CC subfamily.
CC CC -1- SIMILARITY: Contains 2 doublecortin domains.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DB HSSP; AF155819; AAF26673.1; -.
DB HSSP; O63450; 1A06.
DB MBD; MG1; I330861; Dcank1.
DB InterPro; IPR003533; DCX.
DB InterPro; IPR000719; Prot_kinase.
DB InterPro; IPR008271; Ser_thr_pkin_AS.
DB InterPro; IPR002290; Ser_thr_pkinase.
DB Pfam; PF03607; DCX; 2.
DB Pfam; PF00069; pkinase; 1.
DB ProDom; PD000001; Prot_kinase; 1.
DB SMART; SM00537; DCX; 2.
DB SMART; SM00220; S_TKc; 1.
DB PROSITE; PS00309; TC; 2.
DB PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DB PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Neurogenesis.
FT DCKM1 57 143 DOUBLECORTIN 1.
FT DCKM1 186 269 DOUBLECORTIN 2.
FT DCKM1 298 358 SER/PRO-RICH.
FT DCKM1 406 663 PROTEIN_KINASE.
FT NP_BIND 412 420 ATP (BY SIMILARITY).
FT BINDING 435 435 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 756 AA; 84153 MW; 3D1BF18C23129F2 CRC64;

Query Match 21.7%; Score 559; DB 1; Length 756;
Best Local Similarity 35.6%; Pred. No. 1.7e-21;
Matches 119; Conservative 63; Mismatches 128; Indels 24; Gaps 4;

QY 11 KKNYQSEVTDYRDIQGVYKTEEFCEIFRAADKTTGKLTCKKQQRDRGRYKKAANE 70
DB 393 EEGQIPATITERYKKGRTIGDGNFAVVKCIRSTAREVAAKIIKSKRGHEHIGNE 452
QY 71 IGIKKYKHPNIIQLVDVFTKREYFIFFLELATGREFVDMILDOGYSEEDTSNVTRQVL 130
DB 453 VSIIRYKHPNIIQLVDVFTKREYFIFFLELATGREFVDMILDOGYSEEDTSNVTRQVL 512
QY 131 EAVAYLHSLKIVHNLKLENIYVYNRNLKNSKIVISDFHLAKLENGLIKEPGCTPEYLAP 189
DB 513 SAIRYLSLNVTHRDIPENILLASKCKGAFGLATVDDPLTVVCGTPTVYAP 572
QY 190 EWVGRGRYPVDCWAGIYIMYTLISGNPFYEVEEDDYENHDKLPRLIAGDYEDSEPYW 249
DB 573 EIAIFGTYGAKVDIMAGVITYILGCFPF--RSGGDDOE-----VLFQILMGQVDFPS 626
QY 250 PYWDDISAAKDLVTRLMVEVODQRTAEALISEHWISGNAASDKNIKQGVCAQIEKNFA 309
DB 627 PYWDDISAAKELINMMLLVNVDQFSAVGVLEHPWVNDGLPENHQSVAKIKKHEN 686
QY 310 RAKMKKAVVITLTKRLAPBQSTAAQASAT 343
DB 687 -----TGKPSSTAAGSVIAT 703

RESULT 11
DCK1_RAT STANDARD; PRT; 433 AA.
ID DCK1_RAT
AC O08875;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DE 30-MAY-2000 (Rel. 39, last annotation update)
DR Serine/threonine-protein kinase DCAMK1 (EC 2.7.1.1-) (Doublecortin-
DE like and CAM kinase-like 1) (Calcium/calmodulin-dependent protein
DE kinase type 1-like CPG16).
GN DCAMK1 OR CPG16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCST_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar;
RX MEDLINE=9834306; PubMed=9699150;
RA Heyron D., Rattner A., Bundman M., Lederfein D., Gabarras A.,
RA Mangelus M., Silverman M.A., Kedat H., Naor C., Kornuc M., Hanoch T.,
RA Seger R., Theill L.E., Nedivi E., Richter-Levin G., Clitri Y.;
RT "Hippocampal plasticity involves extensive gene induction and multiple
RT cellular mechanisms.";
RL J. Mol. Neurosci. 10:75-98(1998).
CC -I- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
CC SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
CC BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
CC SYSTEM (BY SIMILARITY).
CC -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Camk
CC subfamily.
CC -----
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CC -----
DR EMBL; U78857; AAC9476.1; -.
DR HSSP; O63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0230; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KM Transferase; Serine/threonine-protein kinase; ATP-binding;
KM Neurogenesis.
FT DOMAIN 1 33 SER/PRO-RICH (BY SIMILARITY).
FT DOMAIN 83 340 PROTEIN_KINASE.
FT DOMAIN 391 394 POLY-ARG.
FT NP_BIND 89 ATP (BY SIMILARITY).
FT BINDING 112 112 ATP (BY SIMILARITY).
FT ACT_SITE 204 204 BY SIMILARITY.
SQ SEQUENCE 433 AA; 47680 MW; 0CE5B06B152A557D CRC64;

Query Match 21.6%; Score 558; DB 1; Length 433;
Best Local Similarity 35.7%; Pred. No. 1e-21;
Matches 119; Conservative 62; Mismatches 128; Indels 24; Gaps 4;

QY 12 KNNQPSSEVDRYDLGVYIKTEEFPEIRACDKTTGKGLHTCKKFOKRDGRKRYRAAKNEI 71
DB 71 EGFOIPATITERKYKVGRTIGGNFAVVECEIERSFARBYALKIICKSKCRGKEHMIQNEV 130
QY 72 GILKVVKNPNLQVVDVETREKEYFIFELATNGREVFPMILDGYSRSDTSNVARYOLE 131
DB 131 SILRVKPKPNVYLIEEMDVTEELVYVWELVKGDDLPALITSTSKYTERDASGMLYNLAS 190
QY 132 AVAYIASHIKIVHNTKLENTLVYVYRNLSKSK-IVISDFHATKLENTLIEKPGCTPEYLAPE 190
DB 191 AIKTLHSINIVHRIKPNLENTLVYEHQDSKSLKGDPLGATITVQDPPLVTCGTPPYVAPE 250
QY 191 VVGQRVGRPRVDCNALGVIMITLLSGNPPFEEVBEEDYENHDKLFPKILAGDYEPDSP 250

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Db      251  IIAETGYGKAVDIMAAGVITTYLLCGFPF--RSGBDQ-----VLEFDGLMGQVDFPSS 30
Oy      251  YNDDISQAAKDLYVTLMEVEODQRTTAEBAISHWISGNAASDKNTKDGCAQIEKNFAR 310
Db      305  YMNVSASAKELINMMLVNVDOFSAAQVLEHFWVNDGLFENERQLTSVAGRIKGFN- 363
Oy      311  AKMKKAVRTTLMKRLRAPGSGSTPAAGSASAT 343
Db      364  -----TGPKSSDPAAGSVIAT 390

RESULT 12
KCMB_MOUSE
ID_KCMB_MOUSE STANDARD; PRT; 542 AA.
AC P28657;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II beta chain
DE (AC 2.7.1.123) (Cam-kinase II beta chain) (Cam kinase II beta subunit)
DE (CamK-II beta subunit).
GN CAMK2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=92334366; PubMed=132143;
RA Karls U., Mueller U., Gilbert D.T., Copeland N.G., Jenkins N.A.,
RA Harbers K.;
RT "structure, expression, and chromosome location of the gene for the
RT beta subunit of brain-specific Ca2+/calmodulin-dependent protein
RT kinase II identified by transgene integration in an embryonic lethal
RT mouse mutant".
RL Mol. Cell. Biol. 12:3644-3652(1992).
CC -1- FUNCTION: Cam-kinase II (CAMK2) is a prominent kinase in the
CC central nervous system that may function in long-term potentiation
CC and neurotransmitter release.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Autophosphorylation of CAMK2 plays an important
CC role in the regulation of the kinase activity.
CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
CC gamma, and delta. The different isoforms assemble into homo- or
CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
CC subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X63615; CAA45160.1; -.
CC PIR: A45025; A45025.
CC DR HSSP: Q63450; LA06.
CC MGP: MG1:88257; CamK2b.
CC InterPro: IPR000719; Prot. kinase.
CC InterPro: IPR008271; Ser. Thr. pkin.AS.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PDO00001; Prot_kinase; 1.
CC SMART: SM00107; S_TKc; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
CC PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
CC Transferrin, Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Neurone.
CC DOMAIN 14 272 PROTEIN KINASE.
CC

```

FT NP BIND 20 28 ATP (BY SIMILARITY).
 FT BINDING 43 43 ATP (BY SIMILARITY).
 FT ACT SITE 136 136 BY SIMILARITY.
 FT DOMAIN 291 301 CALMODULIN-BINDING.
 SQ SEQUENCE 542 AA; 60475 MW; 8A7962A62D7075D0 CRC64;

Query Match 21.4%; Score 552; DB 1; Length 542;
 Best Local Similarity 32.7%; Pred. No. 2.6e-21;
 Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDYDGLGVYKTEEFCEIFRAKDKTTG-----KLTCKCKFKQKDRKRYKAANEIGLK 75
 11 TDEYQLEYEDIGKAFSVVRKCYKLTGHEHYAAKIINTKLSARDHOKLEREAK-----ICR 66
 76 MWKHPNITLQVDFVTRKEVFIFLELATGREVDFWILDOGYSESDTSNVVRQVLEAVAY 135
 67 LKHSNIVRLHDSISEGFHYLVFDLVGTGELFEDIVAREYSEADASHCIGQILEAVLH 126
 136 LHSKIVERNLKLENIIVYNNRLKSKIVISDFHLAKLENGLIKE--PCGTPEYLAPEVY 192
 127 CHQMGVVRHDLKRENILLASKCKGAAYKLADFLAIEVQGDQAWFGFAGTPEYLSPEVL 186
 193 GRQRYGPRVDCALIGVIMYLLSGNPFYEEVEDYENHDKLFRKILAGYEPSPYV 252
 187 RKEAYGKRPVDIMACGVILYLLVGYPPFWDE-----DOH--KLXQKIKAGAYDPSPSEW 238
 253 DISQAQKDLVTRLMVEEDQORITAEASISHEMI--SGNAAADKNIKDGVC-CAQIEKNFA 309
 239 DVTPEAKNLINQMLTINPAKRIITAEHALKHPVOCRSIVASMERQETVEC--LKQFNA 296
 310 RAKWKKAIVRTTLMKRLAPESGSTAAQASATDTATPGAGATPAAASGATSAPEGD 369
 297 RRLKGAIIITMLATRNFSVGRQTAPATMST-----AASGTMGLVEQAKSLN-- 346
 370 AARAAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDSITPATDGS 417
 347 ----KKADGVKPTNS--TKNSSAITSFKGSLPPALPEQTIVINPVDG-IKESSDST 398
 418 VTPVTRSATPATDGRATPATSESTVPTTQ 447
 399 NTTIEDEDA-----KARKOEIIKITE 419

RESULT 13

KCCB_RAT STANDARD; PRT; 542 AA.

AC P08413; 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II beta chain
 DE (EC 2.7.1.423) (Cam-Kinase II beta chain) (Cam kinase II beta subunit)
 DE (CamK-II beta subunit).
 GN CAMK2B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN (1) _____
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87175563; PubMed=3470758;
 RA Bernett M.K., Kennedy M.B.;
 RT "Deduced primary structure of the beta subunit of brain type II
 RT Ca2+/calmodulin-dependent protein kinase determined by molecular
 RT cloning";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1794-1798(1987).
 CC -1- FUNCTION: Cam-kinase II (CAMK2) is a prominent kinase in the
 CC central nervous system that may function in long-term potentiation
 CC and neurotransmitter release.
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ENZYME REGULATION: Autophosphorylation of CAMK2 plays an important
 CC role in the regulation of the kinase activity.

CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
 CC gamma, and delta. The different isoforms assemble into homo- or
 CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
 CC subfamily.

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CC EMBL; M16112; AAA1866.1; --
 DR PIR; A26464; A26464.
 DR HSRP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc_1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Neurone.
 FT DOMAIN 14 272
 FT NP_BIND 20 28
 FT BINDING 43 43 ATP (BY SIMILARITY).
 FT ACT SITE 136 136 BY SIMILARITY.
 FT DOMAIN 291 301 CALMODULIN-BINDING.
 FT SEQUENCE 542 AA; 60401 MW; 8A7962A64A930D0 CRC64;

Query Match 21.3%; Score 551; DB 1; Length 542;
 Best Local Similarity 32.7%; Pred. No. 3e-21;
 Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDYDGLGVYKTEEFCEIFRAKDKTTG-----KLTCKCKFKQKDRKRYKAANEIGLK 75
 11 TDEYQLEYEDIGKAFSVVRKCYKLTGHEHYAAKIINTKLSARDHOKLEREAK-----ICR 66
 76 MWKHPNITLQVDFVTRKEVFIFLELATGREVDFWILDOGYSESDTSNVVRQVLEAVAY 135
 67 LKHSNIVRLHDSISEGFHYLVFDLVGTGELFEDIVAREYSEADASHCIGQILEAVLH 126
 136 LHSKIVERNLKLENIIVYNNRLKSKIVISDFHLAKLENGLIKE--PCGTPEYLAPEVY 192
 127 CHQMGVVRHDLKRENILLASKCKGAAYKLADFLAIEVQGDQAWFGFAGTPEYLSPEVL 186
 193 GRQRYGPRVDCALIGVIMYLLSGNPFYEEVEDYENHDKLFRKILAGYEPSPYV 252
 187 RKEAYGKRPVDIMACGVILYLLVGYPPFWDE-----DOH--KLXQKIKAGAYDPSPSEW 238
 253 DISQAQKDLVTRLMVEEDQORITAEASISHEMI--SGNAAADKNIKDGVC-CAQIEKNFA 309
 239 DVTPEAKNLINQMLTINPAKRIITAEHALKHPVOCRSIVASMERQETVEC--LKQFNA 296
 310 RAKWKKAIVRTTLMKRLAPESGSTAAQASATDTATPGAGATPAAASGATSAPEGD 369
 297 RRLKGAIIITMLATRNFSVGRQTAPATMST-----AASGTMGLVEQAKSLN-- 346
 370 AARAAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDSITPATDGS 417
 347 ----KKADGVKPTNS--TKNSSAITSFKGSLPPALPEQTIVINPVDG-IKESSDST 398
 418 VTPVTRSATPATDGRATPATSESTVPTTQ 447
 399 NTTIEDEDA-----KARKOEIIKITE 419

RESULT 14

KCCG RAT STANDARD; PRT; 527 AA.

AC P11730; 064003; 064004;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II gamma chain
 DE (EC 2.7.1.123) (Cam-kinase II gamma chain) (Cam kinase II gamma
 subunit) (CaMK-II gamma subunit).
 GN CAMK2G.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=89034067; PubMed=2846534;
 RA Tanimatsu T., Kameshita I., Fujisawa H.;
 RT "Molecular cloning of the cDNA encoding the third polypeptide (gamma)
 of brain calmodulin-dependent protein kinase II.";
 RL J. Biol. Chem. 263:16082-16086(1988).
 RT Biochem. J. 299:489-495(1994).
 CC -1- FUNCTION: Cam-kinase II (CaMK2) is a prominent kinase in the
 central nervous system that may function in long-term potentiation
 and neurotransmitter release.
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ENZYME REGULATION: Autophosphorylation of CaMK2 plays an important
 role in the regulation of the kinase activity.
 CC -1- SUBUNIT: CaMK2 is composed of four different chains: alpha, beta,
 gamma, and delta. The different isoforms assemble into homo- or
 heteromultimeric holoenzymes composed of 8 to 12 subunits.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=A;
 CC IsoId=P11730-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P11730-2; Sequence=VSP_004781, VSP_004782;
 CC Name=C;
 CC IsoId=P11730-3; Sequence=VSP_004781, VSP_004783;
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
 subfamily.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 or send an email to license@ebi.ac.uk).

KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
 FT DOMAIN 14 272
 FT NP_BIND 20 28
 FT BINDING 43 43
 FT ACT_SITE 136 136
 FT DOMAIN 291 301
 FT VARSPPLIC 316 336
 FT VARSPPLIC 351 361
 FT VARSPPLIC 351 361
 FT VARSPPLIC 352 362
 FT VARSPPLIC 352 362
 FT CONFLICT 2 2
 FT SEQUENCE 527 AA; 59038 MW; 58DBF1B72F64FA31 CRC64;
 SQ
 Query Match 21.0%; Score 542; DB 1; Length 527;
 Best Local Similarity 34.4%; Pred. No. 8.2e-21;
 Matches 141; Conservative 77; Mismatches 146; Indels 46; Gaps 13;
 QY 21 TDRYDLGVIVKITEEFCEIFRAKDTT-----GKLTCKKFKRDKRKVKAKNEIGILK 75
 DB 11 TDDYQLFEELGKAPSVVRCKVKTSTQEVAAKINTKLSARPHQKLEARE-----ICR 66
 QY 76 MKKPNIIQLVDVFTKREYFIELATGREVPWILDQGYISERDTSNVYRQVLENAV 135
 DB 67 LKHPNIVRLHDSISEGPHVLPVLTGGLFEDIVAREYSEADASHCHQILSEVNH 126
 QY 136 LHSIKIVRNKLENTLVYVNRSLKNSKIYISDFHLAKLENGIKSP-----CGTPEYIAP 189
 DB 127 IHQHDIVRHDLKPELNLASKCKGAAYKLADFGLAIEVQG---EQQAFGAGTDPGYISP 183
 QY 190 EVVGRQRYGRPYDCWAIVIMTLLSGNPPEYEEVEDYENHDKLPRKLIAGDEPDS 249
 DB 184 EYLRKDPYKPKPDVIAAGVILYLLVGPFPWDE-----DQH--KLYQQLKAGAYDPFS 235
 QY 250 PYWDDISQAKDLVTRLMVEBODQRTLEBAISHWT--SGNAASDKNIKGV-CAQLEK 306
 DB 236 PEMDTVTPEAKKLINQMILINPAKITADQALKHPWCORSTVASMGRQETVEC--LRK 293
 QY 307 NPARAKMKKAVRVITLMGR-LRAPQSTAAQASADTDTPGAAGATAAASGATSA 365
 DB 294 FVARRKLKGAITITTLVSRNFSVGRQSSAPASPAAS-----AAGLAGQAAASLANKK 345
 QY 366 PEGDABARAKSDNVAPADRSATPATDGSATPATDGSATTPATD 415
 DB 346 SDGIVKXKSSSVHLMPEQTIVN-----ATDG-INGTSBSCNTTDD 389
 RESULT 15
 KCCA HUMAN STANDARD; PRT; 478 AA.
 AC Q9UQW7; Q9Y352;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II alpha chain
 DE (EC 2.7.1.123) (Cam-kinase II alpha chain) (Cam kinase II alpha
 subunit) (CaMK-II alpha subunit).
 GN CAMK2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE=Brain;
 RA Li G.Y., Cooper N.G.F.;
 RT "Human calcium/calmodulin-dependent protein kinase II: cDNA cloning
 and gene analysis.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

central nervous system that may function in long-term potentiation
and neurotransmitter release.
CC CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Autophosphorylation of Thr-286 allows the
CC kinase to switch from a calmodulin-dependent to a calmodulin-
CC independent state (By similarity).
CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
CC gamma, and delta. The different isoforms assemble into homo- or
CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=C9UCM7-1; Sequence=Displayed;
CC Name=B;
CC IsoId=C9UCM7-2; Sequence=VSP 004766;
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL; AF145710; AAD30558.1; -;
CC EMBL; AF145711; AAD30559.1; -;
CC HSSP; O63450; 1A06.
CC DR Genew; HGNC:1460; CAMK2A.
CC MIM; 114078; -;
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR008271; Ser_Thr_kin_AS.
CC DR InterPro; IPR002290; Ser_Thr_kinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00220; S_TKc; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC KM Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
CC KM Phosphorylation; ATP-binding; Alternative splicing.
CC FT DOMAIN 13 271 PROTEIN KINASE.
CC FT NP_BIND 19 27 ATP (BY SIMILARITY).
CC FT BINDING 42 42 ATP (BY SIMILARITY).
CC FT ACT_SITE 135 135 BY SIMILARITY.
CC FT MOD_RES 286 286 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC FT DOMAIN 290 300 CALMODULIN-BINDING.
CC FT VARSPIC 328 328 K -> KKKSSSVQLM (in isoform B).
CC FT /FTId=VSP_004766.
CC SQ SEQUENCE 478 AA; 54029 MW; 10800A85CAD724BB CRC64;
Query Match 20.84; Score 537; DB 1; Length 478;
Best Local Similarity 32.34; Pred. No. 1.3e-20;
Matches 137; Conservative 74; Mismatches 141; Indels 72; Gaps 12;
QY 21 TDRYDLDGVITKEEFCHFR-----AKDKTTGKLTCKFKQKDGKRVKRAANEIGILK 75
DB 10 TEEYQLEELGKGFVVRRCVYKLAGQYAAKIINTKLSARDHQLEREAR-----ICR 65
QY 76 MTKAPNLTQVDVFTVTKKEFIFLELATGREVDWILDGYSERDTSNVVROULEAVAY 135
DB 66 LKXHPNIVRLHDS;SERGHHYLLFDLVYTGELFEDIYAREYSEADSHCTIQILRAVLA 125
QY 136 LHSKIVHRNKLKENTLYYVRKLNKSKIVISDFHLAKLNLKLEP-----CGTPEYLAP 189
DB 126 CHQGVVVRHDLKPEKPNLLASLKGAAYKADFGIALIVEG--EQAMRFGATPGYLS 182
QY 190 EVVGRQRYGRPVDCMAGIVMYILLGNPPYEEVEEDDYENDKILFRKILAGDYEFDS 249
DB 183 EVLRKDKYGRKVDLMACGVILYLLVGVPPFWDE-----DQH--RLYQGIKAGAYDFPS 234

DB 235 PEMDVTTPPAKDLINKMLTINSKRTITAAFLKHPWISHRSVASCWERQETVDC--LKK 292
QY 307 NFAAKKKKAVVTTLMKRLRAPESSTPAASASATDTATPGAAAGATMAAASGATSAP 366
DB 293 FNAERRLKGAILTTLW-----ATNFSGKSGG----- 320
QY 367 EGDARAAASDVAAADRSATPATDGSATPATDGSVTPATDGSITPATDG---SVTPYTD 423
DB 321 -----NKSIDGVKSSSESTNTTIDEDTKVAKKEIKVTEQLIAISNGPFESTIKCD 374
QY 424 RSAT 427
DB 375 PGMT 378

Search completed: April 23, 2004, 15:48:43
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:49:49 ; Search time 48 Seconds

(without alignments)
2885.710 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581

Sequence: 1 MPFGCTTLDKKNYNQPSREV.....SSKGERAAGYAGDSQREAS 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgnt2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgnt2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
3: /cgnt2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgnt2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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6: /cgnt2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgnt2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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16: /cgnt2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgnt2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgnt2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2581	100.0	501	12	US-10-669-689-2
2	2581	100.0	501	13	US-10-153-921-2
3	2577	99.8	501	9	US-09-797-039-2
4	2577	99.8	501	12	US-10-423-643-19
5	2577	99.8	501	14	US-10-170-789-2
6	2577	99.8	501	15	US-10-085-198-6
7	2577	99.8	501	15	US-10-258-106-17
8	2402.5	93.1	473	12	US-10-425-114-54473
9	2402.5	93.1	473	12	US-10-425-114-54473
10	1457.5	56.5	317	12	US-10-425-114-54471
11	966	37.4	204	11	US-09-764-875-725
12	852	33.0	219	9	US-09-764-868-832
13	852	33.0	219	11	US-09-764-875-1035
14	793	30.7	370	9	US-09-817-181-4
15	793	30.7	370	10	US-09-769-970-19

16	793	30.7	370	14	US-10-142-356-7	Sequence 7, Appl
17	793	30.7	370	14	US-10-300-828-4	Sequence 4, Appl
18	793	30.7	370	14	US-10-090-002-4	Sequence 4, Appl
19	793	30.7	370	14	US-10-204-041-10	Sequence 10, Appl
20	771	29.9	317	14	US-09-935-864-36	Sequence 36, Appl
21	771	29.9	317	14	US-10-125-835-36	Sequence 36, Appl
22	771	29.9	357	14	US-10-024-0368-2	Sequence 2, Appl
23	771	29.9	357	15	US-10-258-106-2	Sequence 2, Appl
24	767.5	29.7	385	15	US-10-446-175-2	Sequence 2, Appl
25	764	29.6	355	14	US-10-355-975-10	Sequence 10, Appl
26	764	29.6	355	15	US-10-258-106-11	Sequence 11, Appl
27	754.5	29.2	356	15	US-10-446-175-4	Sequence 4, Appl
28	747.5	29.0	476	10	US-09-935-864-5	Sequence 5, Appl
29	747.5	29.0	476	12	US-09-960-643-2	Sequence 4, Appl
30	747.5	29.0	476	12	US-10-380-235-5	Sequence 4, Appl
31	747.5	29.0	476	14	US-10-125-835-5	Sequence 5, Appl
32	746	28.9	460	10	US-09-935-864-3	Sequence 3, Appl
33	746	28.9	460	14	US-10-125-835-3	Sequence 3, Appl
34	718	27.8	326	9	US-09-817-181-2	Sequence 2, Appl
35	718	27.8	326	14	US-10-300-828-2	Sequence 2, Appl
36	718	27.8	326	14	US-10-090-002-2	Sequence 2, Appl
37	699.5	27.1	484	12	US-10-425-114-54130	Sequence 16, Appl
38	650	25.2	280	9	US-09-835-788A-16	Sequence 16, Appl
39	650	25.2	280	14	US-10-175-042-16	Sequence 16, Appl
40	645.5	25.0	310	15	US-10-369-493-5955	Sequence 5955, Ap
41	642.5	24.9	343	10	US-09-769-970-5	Sequence 5, Appl
42	608	23.6	473	14	US-10-320-351-15	Sequence 15, Appl
43	608	23.6	473	15	US-10-116-275-153	Sequence 153, App
44	607	23.5	298	12	US-10-220-120-240	Sequence 240, App
45	584.5	22.6	424	12	US-10-072-012-330	Sequence 330, App

ALIGNMENTS

RESULT 1	US-10-669-689-2	Application US/10669689
1	Sequence 2, Appl	Publication No. US20040038363A1
2	Sequence 2, Appl	GENERAL INFORMATION:
3	Sequence 2, Appl	APPLICANT: VAN, Chunhua et al.
4	Sequence 2, Appl	TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
5	Sequence 2, Appl	TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
6	Sequence 2, Appl	FILE REFERENCE: CLO00612DVI1
7	Sequence 2, Appl	CURRENT APPLICATION NUMBER: US/10/669,689
8	Sequence 2, Appl	CURRENT FILING DATE: 2003-09-25
9	Sequence 2, Appl	PRIOR APPLICATION NUMBER: 09/734,030
10	Sequence 2, Appl	PRIOR FILING DATE: 2000-12-12
11	Sequence 2, Appl	PRIOR APPLICATION NUMBER: 60/207,281
12	Sequence 2, Appl	PRIOR FILING DATE: 2000-05-30
13	Sequence 2, Appl	NUMBER OF SEQ ID NOS: 3
14	Sequence 2, Appl	SOFTWARE: fastseq for Windows Version 4.0
15	Sequence 2, Appl	SEQ ID NO: 2
16	Sequence 2, Appl	LENGTH: 501
17	Sequence 2, Appl	TYPE: PRT
18	Sequence 2, Appl	ORGANISM: Homo sapiens
19	Sequence 2, Appl	US-10-669-689-2
20	Sequence 2, Appl	Query Match
21	Sequence 2, Appl	Best Local Similarity 100.0%; Score 2581; DB 12; Length 501;
22	Sequence 2, Appl	Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
24	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
25	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
26	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
27	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
28	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
29	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
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32	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
33	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
34	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
35	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
36	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
37	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
38	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
39	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
40	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
41	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
42	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
43	Sequence 2, Appl	1 MPFGCTTLDKKNYNQPSREVTDRLGVYIKTEECETFRADKTTGKLTCKKQKDG 60
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Db 181 CGTPEYLAPEVVGROGRYPVDCMAIGVIMYILLSGNPPEYEEVEDDYENHDKLFRKI 240
Qy 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
Db 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
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Db 421 VTDRSATPATDGRATPATTEESTVPTTQSSAMLTAKAAATPEBMAQPDSTAPEGATGOAP 480
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Db 481 PSSKGEBAAGYAQESQREAS 501

RESULT 2

US-10-153-921-2
; Sequence 2, Application US/10153921
; Publication No. US20020142430A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000612D1V
; CURRENT APPLICATION NUMBER: US/10/153,921
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-153-921-2

Query Match 100.0%; Score 2581; DB 13; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.8e-160;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPFGCVTLGDKNKYNQSEVTDRIYDLGOVITKEEFCEIFRAKDKTGKLTCKKFKQKRG 60
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Db 61 RKTKAKAKNEIGILKWKVKNHNIQLVDVFTYTRKEVYIFLELATGREVFWILDQGYYSER 120
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Qy 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
Db 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300

Db 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
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Qy 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
Db 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
Qy 421 VTDRSATPATDGRATPATTEESTVPTTQSSAMLTAKAAATPEBMAQPDSTAPEGATGOAP 480
Db 421 VTDRSATPATDGRATPATTEESTVPTTQSSAMLTAKAAATPEBMAQPDSTAPEGATGOAP 480
Qy 481 PSSKGEBAAGYAQESQREAS 501
Db 481 PSSKGEBAAGYAQESQREAS 501

RESULT 3

US-09-797-039-2
; Sequence 2, Application US/09797039
; Patent No. US20020042099A1
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
; TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
; FILE REFERENCE: 10448-017001
; CURRENT APPLICATION NUMBER: US/09/797,039
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-797-039-2

Query Match 99.8%; Score 2577; DB 9; Length 501;
Best Local Similarity 99.8%; Pred. No. 3.3e-160;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPFGCVTLGDKNKYNQSEVTDRIYDLGOVITKEEFCEIFRAKDKTGKLTCKKFKQKRG 60
Db 1 MPFGCVTLGDKNKYNQSEVTDRIYDLGOVITKEEFCEIFRAKDKTGKLTCKKFKQKRG 60
Qy 61 RKTKAKAKNEIGILKWKVKNHNIQLVDVFTYTRKEVYIFLELATGREVFWILDQGYYSER 120
Db 61 RKTKAKAKNEIGILKWKVKNHNIQLVDVFTYTRKEVYIFLELATGREVFWILDQGYYSER 120
Qy 121 DTSNVVRQVLEAAVYHLSKIVHRNKLKLENTLVYNNRLKNSKTVISDFHLAKLENGLKEP 180
Db 121 DTSNVVRQVLEAAVYHLSKIVHRNKLKLENTLVYNNRLKNSKTVISDFHLAKLENGLKEP 180
Qy 181 CGTPEYLAPEVVGROGRYPVDCMAIGVIMYILLSGNPPEYEEVEDDYENHDKLFRKI 240
Db 181 CGTPEYLAPEVVGROGRYPVDCMAIGVIMYILLSGNPPEYEEVEDDYENHDKLFRKI 240
Qy 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
Db 241 LAGDYEFDSYPWMDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKDG 300
Qy 301 CAQIEKNFAPAKKAVRVTTLMKRLAPESQSTAAQASATDTATPGAGATATAAAS 360
Db 301 CAQIEKNFAPAKKAVRVTTLMKRLAPESQSTAAQASATDTATPGAGATATAAAS 360
Qy 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
Db 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420

Thu Apr 29 08:44:18 2004

us-10-669-689-2.rapb

Page 3

QY 421 VTRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
DB 421 ATBRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 481 PSSKGEBAAGYAQESQREAS 501

RESULT 4
US-10-423-543-19
; Sequence 19, Application US/10423543
; Publication No. US20040056355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Cutler, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williams, Mark J.
; APPLICANT: Siles-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
; TITLE OF INVENTION: 18610, 33217, 21967, 11983, 36555 OR 593 MOLECULES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MP103-0230NIM
; CURRENT APPLICATION NUMBER: US/10/423, 543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278, 036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711, 216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205, 447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012, 055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248, 325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003, 690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248, 893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797, 039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186, 061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217, 168
; PRIOR FILING DATE: 2002-08-12
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-423-543-19

Query Match 99.8%, Score 2577, DB 12, Length 501,
Best Local Similarity 99.8%, Pred. No. 3,35-160,
Matches 500, Conservative 0, Mismatches 1, Indels 0, Gaps 0,

QY 1 MPFGCVTLGDKKNNQBPSEVTDRLDQVYKTEEFCEIFPAKDKTKTKTKCKKFGQRDG 60
DB 1 MPFGCVTLGDKKNNQBPSEVTDRLDQVYKTEEFCEIFPAKDKTKTKTKCKKFGQRDG 60
QY 61 RKVKAAKNEIGILKMGVGHPIILQVDFVTRKEYFIFLELATGREVDMILDOGYSER 120

DB 61 RKVKAAKNEIGILKMGVGHPIILQVDFVTRKEYFIFLELATGREVDMILDOGYSER 120
QY 121 DTSNVRQVLEAVAIHSLKTVHRLKLENVYNNRLKNSKIVSDFLATLGNGLIEP 180
DB 121 DTSNVRQVLEAVAIHSLKTVHRLKLENVYNNRLKNSKIVSDFLATLGNGLIEP 180
QY 181 CGTPEYLAPEVVGRORYGRPVDCMAIGVIMYILSGNPFEEVEEDDYENHDKLFRKI 240
DB 181 CGTPEYLAPEVVGRORYGRPVDCMAIGVIMYILSGNPFEEVEEDDYENHDKLFRKI 240
QY 241 IAGDYEFDSPYWDDISQAKDLVTRLMVEVODRITTEEAISHENISGNAASDKNIKGV 300
DB 241 IAGDYEFDSPYWDDISQAKDLVTRLMVEVODRITTEEAISHENISGNAASDKNIKGV 300
QY 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPESSTIAAOSASATDTATGAAAGATAAAS 360
DB 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPESSTIAAOSASATDTATGAAAGATAAAS 360
QY 361 GATSAPEGDAAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPA 420
DB 361 GATSAPEGDAAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPA 420
QY 421 VTRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
DB 421 ATBRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 481 PSSKGEBAAGYAQESQREAS 501

RESULT 5
US-10-170-789-2
; Sequence 2, Application US/10170789
; Publication No. US20030180930A1
; GENERAL INFORMATION:
; APPLICANT: Rachel E. Meyers
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-191001
; CURRENT APPLICATION NUMBER: US/10/170, 789
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797, 039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186, 061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882, 166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212, 078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934, 406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226, 740
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/861, 801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16549
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205, 508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/801, 267
; PRIOR FILING DATE: 2001-03-06

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/ PRIOR APPLICATION NUMBER: PCT/US01/07138
/ PRIOR FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: US 60/187,454
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/829,671
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: PCT/US01/40483
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: US 60/197,508
/ PRIOR FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 09/961,721
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: PCT/US01/29904
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: US 60/235,023
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US 10/045,367
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US 60/246,561
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: US 09/801,275
/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: PCT/US01/07074
/ PRIOR FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: US 60/187,420
/ PRIOR FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-170-789-2
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Query Match 99.8%; Score 2577; DB 14; Length 501;

Best Local Similarity 99.8%; Pred. No. 3.3e-160; Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MPEGCVTLDGKKNYNPSEVTDRLDGVYKTEFCEIFPAKDKTGTCKKFKRQD 60
DB 1 MPEGCVTLDGKKNYNPSEVTDRLDGVYKTEFCEIFPAKDKTGTCKKFKRQD 60
QY 61 RKTKRAAKNEIGILKWKHPNLIQLVDVFTYRKEVYIFLELATGRVFPWILDQYYSER 120
DB 61 RKTKRAAKNEIGILKWKHPNLIQLVDVFTYRKEVYIFLELATGRVFPWILDQYYSER 120
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLKLENTLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLKLENTLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
QY 181 CGPEYLAPEVVGROGRGVPCVDCMAIGVIMYILLSGNPPFEVEEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGROGRGVPCVDCMAIGVIMYILLSGNPPFEVEEDDYENHDKNLFKRI 240
QY 241 LAGDYFEDSPYWDISQAADLVTRLMVEVQDORITAEBAISHWISGNAASDKNIKQGV 300
DB 241 LAGDYFEDSPYWDISQAADLVTRLMVEVQDORITAEBAISHWISGNAASDKNIKQGV 300
QY 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSSTAQAQASATDTATPPAAGATTAAS 360
DB 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSSTAQAQASATDTATPPAAGATTAAS 360
QY 361 GATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTPATDGSVTP 480
DB 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTPATDGSVTP 480
QY 481 PSSKGEBAAGYAOESQREAS 501
DB 481 PSSKGEBAAGYAOESQREAS 501
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RESULT 6
US-10-085-198-6

/ Sequence 6, Application US/10085198
/ Publication No. US20040009907A1

/ GENERAL INFORMATION:

/ APPLICANT: Alcobrook et al.

/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

/ FILE REFERENCE: 21402-279
/ CURRENT APPLICATION NUMBER: US/10/085,198

/ PRIOR FILING DATE: 2002-02-25

/ PRIOR APPLICATION NUMBER: 60/271,646

/ PRIOR FILING DATE: 2001-02-26

/ PRIOR APPLICATION NUMBER: 60/276,401

/ PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: 60/311,981

/ PRIOR FILING DATE: 2001-08-13

/ PRIOR APPLICATION NUMBER: 60/312,858

/ PRIOR FILING DATE: 2001-08-16

/ PRIOR APPLICATION NUMBER: 60/271,840

/ PRIOR FILING DATE: 2001-02-27

/ PRIOR APPLICATION NUMBER: 60/277,324

/ PRIOR FILING DATE: 2001-03-20

/ PRIOR APPLICATION NUMBER: 60/286,096

/ PRIOR FILING DATE: 2001-04-21

/ PRIOR APPLICATION NUMBER: 60/299,695

/ PRIOR FILING DATE: 2001-06-20

/ PRIOR APPLICATION NUMBER: 60/315,614

/ PRIOR FILING DATE: 2001-08-29

/ PRIOR APPLICATION NUMBER: 60/272,405

/ PRIOR FILING DATE: 2001-02-28

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 653

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 6

/ LENGTH: 501

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-085-198-6

Query Match 99.8%; Score 2577; DB 15; Length 501;

Best Local Similarity 99.8%; Pred. No. 3.3e-160; Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MPEGCVTLDGKKNYNPSEVTDRLDGVYKTEFCEIFPAKDKTGTCKKFKRQD 60
DB 1 MPEGCVTLDGKKNYNPSEVTDRLDGVYKTEFCEIFPAKDKTGTCKKFKRQD 60
QY 61 RKTKRAAKNEIGILKWKHPNLIQLVDVFTYRKEVYIFLELATGRVFPWILDQYYSER 120
DB 61 RKTKRAAKNEIGILKWKHPNLIQLVDVFTYRKEVYIFLELATGRVFPWILDQYYSER 120
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLKLENTLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLKLENTLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
QY 181 CGPEYLAPEVVGROGRGVPCVDCMAIGVIMYILLSGNPPFEVEEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGROGRGVPCVDCMAIGVIMYILLSGNPPFEVEEDDYENHDKNLFKRI 240
QY 241 LAGDYFEDSPYWDISQAADLVTRLMVEVQDORITAEBAISHWISGNAASDKNIKQGV 300
DB 241 LAGDYFEDSPYWDISQAADLVTRLMVEVQDORITAEBAISHWISGNAASDKNIKQGV 300
QY 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSSTAQAQASATDTATPPAAGATTAAS 360
DB 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSSTAQAQASATDTATPPAAGATTAAS 360
QY 361 GATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDARAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
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QY 421 VTDRSATPATDGRATPATPEESTVPTTQSSAMLATYAAATPEPMAAOPDSTAPEGATGQAP 480
Db 421 ATDRSATPATDGRATPATPEESTVPTTQSSAMLATYAAATPEPMAAOPDSTAPEGATGQAP 480
QY 481 PSSKGEAAGYAQESQREAS 501
Db 481 PSSKGEAAGYAQESQREAS 501

RESULT 7

US-10-258-106-17
; Sequence 17, Application US/10258106
; Publication No. US20040018185A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; TRIBOULEY, Catherine M.
; APPLICANT: KEARNEY, Liam; GRIFFIN, Jennifer A.
; APPLICANT: NGUYEN, Daniel B.; BANDMAN, Olga
; APPLICANT: LU, Dying Aina M.; LAU, Preeti G.
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.
; APPLICANT: WALIA, Narinder K.; YAO, Monique G.
; APPLICANT: PATTERSON, Chandra; BURRILL, John D.
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.
; APPLICANT: RECIPON, Shirley A.; LU, Yan
; APPLICANT: TANG, Y. Tom; HAFALIA, April J.A.
; APPLICANT: ELIOT, Vicki S.; BAUGHN, Mariah R.
; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi
; APPLICANT: BOROWSKY, Mark L.; AU-YOUNG, Janice K.
; APPLICANT: HILLMAN, Jennifer L.; GURUFARJAN, Rajagopal
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0076 USN
; CURRENT APPLICATION NUMBER: US/10/258,106
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/12392
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/199,021
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/200,226
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,339
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/203,505
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/205,654
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/207,739
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/208,795
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040018185A1 71584520CD1
US-10-258-106-17

Query Match 99.8%; Score 2577; DB 15; Length 501;
Best Local Similarity 99.8%; Pred. No. 3.3e-160;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPFGCVTLGSKKNYNQSEVYTDRLDGLGVITKEEFCIFRAKDKTTGKLTCKKFKQKRDG 60
Db 1 MPFGCVTLGSKKNYNQSEVYTDRLDGLGVITKEEFCIFRAKDKTTGKLTCKKFKQKRDG 60
QY 61 RKVRKAANKNEIGILKMKVKNHNIQLVDVFTTRKEYFFLELATGREVFWILDQGYYSER 120
Db 61 RKVRKAANKNEIGILKMKVKNHNIQLVDVFTTRKEYFFLELATGREVFWILDQGYYSER 120

QY 121 DTSNVROVLBAVAVYLSIKIVHRNKLKLENTVYVNRKSKIVISDFILAKLENGLIKPEP 180
Db 121 DTSNVROVLBAVAVYLSIKIVHRNKLKLENTVYVNRKSKIVISDFILAKLENGLIKPEP 180
QY 181 CGTPEYLAPEVVGQRQYGRPVDCWAGIVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
Db 181 CGTPEYLAPEVVGQRQYGRPVDCWAGIVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
QY 241 LAGDYEFDSPYWDDISQAQKDLVTRLMVEYQDQRTAEALISHEMISGNAADKRIKQGV 300
Db 241 LAGDYEFDSPYWDDISQAQKDLVTRLMVEYQDQRTAEALISHEMISGNAADKRIKQGV 300
QY 301 CAQIEKNFARAKKCAVRRITLMKRLRAPESSTYAAQASATDTPATPAGATPAAAS 360
Db 301 CAQIEKNFARAKKCAVRRITLMKRLRAPESSTYAAQASATDTPATPAGATPAAAS 360
QY 361 GATSAPBGPABAAKSDNVAAPADRSATPATDGSATPATDGSITPATDGSVTP 420
Db 361 GATSAPBGPABAAKSDNVAAPADRSATPATDGSATPATDGSITPATDGSVTP 420
QY 421 VTDRSATPATDGRATPATPEESTVPTTQSSAMLATYAAATPEPMAAOPDSTAPEGATGQAP 480
Db 421 ATDRSATPATDGRATPATPEESTVPTTQSSAMLATYAAATPEPMAAOPDSTAPEGATGQAP 480
QY 481 PSSKGEAAGYAQESQREAS 501
Db 481 PSSKGEAAGYAQESQREAS 501

RESULT 8

US-10-425-114-54473
; Sequence 34473, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54473
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-060-E3_FLI.pap
US-10-425-114-54473

Query Match 93.1%; Score 2402.5; DB 12; Length 473;
Best Local Similarity 93.6%; Pred. No. 7.6e-149;
Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKNYNQSEVYTDRLDGLGVITKEEFCIFRAKDKTTGKLTCKKFKQKRDG 60
Db 4 MPFGCVTLGDKKNYNQSEVYTDRLDGLGVITKEEFCIFRAKDKTTGKLTCKKFKQKRDG 63
QY 61 RKVRKAANKNEIGILKMKVKNHNIQLVDVFTTRKEYFFLELATGREVFWILDQGYYSER 120
Db 64 RKVRKAANKNEIGILKMKVKNHNIQLVDVFTTRKEYFFLELATGREVFWILDQGYYSER 123
QY 121 DTSNVROVLBAVAVYLSIKIVHRNKLKLENTVYVNRKSKIVISDFILAKLENGLIKPEP 180
Db 124 DTSNVROVLBAVAVYLSIKIVHRNKLKLENTVYVNRKSKIVISDFILAKLENGLIKPEP 183
QY 181 CGTPEYLAPEVVGQRQYGRPVDCWAGIVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
Db 184 CGTPEYLAPEVVGQRQYGRPVDCWAGIVIMYILLSGNPFYEVEEDDYENHDKLFRKI 243

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QY 241 LAGDYEFDSBPYWDLSQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGV 300
DB 244 LAGDYEFDSBPYWDLSQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGV 303
QY 301 CAQIEKNFARAKKKAIVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 360
DB 304 CAQIEKNFARAKKKAIVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 353
QY 361 GATSABEGDAPARAASDUNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 354 -----ADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 392
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 480
DB 393 ATDRSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 452
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 453 PSSKGEBAAGYAQESQREAS 473

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RESULT 9

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US-10-425-114-54513
; Sequence 54513, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54513
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-022-E3_F11.pcp
US-10-425-114-54513

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Query Match 93.1%; Score 2402.5; DB 12; Length 473;
 Best Local Similarity 93.6%; Pred. No. 7.6e-149;
 Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

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QY 1 MPFGCTTLDGKKNYNSPSEVTDRYDGOYIKTEBEFETIRADOKTTGKLTHTKKQKDG 60
DB 4 MPFGCTTLDGKKNYNSPSEVTDRYDGOYIKTEBEFETIRADOKTTGKLTHTKKQKDG 63
QY 61 RKRKAAKKEIGILKNVKNPNILQVDVFTVRKEVITFELATGRFVPMILDOGYYSR 120
DB 64 RKRKAAKKEIGILKNVKNPNILQVDVFTVRKEVITFELATGRFVPMILDOGYYSR 123
QY 121 DTSNVVROYLVAAYLHSLKIVHRNLKLENLVYNNRKNKSKIVISDFHLAKLENGLIKEP 180
DB 124 DTSNVVROYLVAAYLHSLKIVHRNLKLENLVYNNRKNKSKIVISDFHLAKLENGLIKEP 183
QY 181 CGTPEYLAEBVVGKRGKVPDCAIGVIMYILSGNPPFYEEVEDDYENHDKULFRKI 240
DB 184 CGTPEYLAEBVVGKRGKVPDCAIGVIMYILSGNPPFYEEVEDDYENHDKULFRKI 243
QY 241 LAGDYEFDSBPYWDLSQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGV 300
DB 244 LAGDYEFDSBPYWDLSQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGV 303
QY 301 CAQIEKNFARAKKKAIVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 360

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DB 304 CAQIEKNFARAKKKAIVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 353
QY 361 GATSABEGDAPARAASDUNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 354 -----ADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 392
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 480
DB 393 ATDRSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 452
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 453 PSSKGEBAAGYAQESQREAS 473

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RESULT 10

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US-10-425-114-54471
; Sequence 54471, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54471
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4676-058-A2_F11.pcp
US-10-425-114-54471

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Query Match 56.5%; Score 1457.5; DB 12; Length 317;
 Best Local Similarity 94.8%; Pred. No. 2.4e-97;
 Matches 291; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

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QY 196 RYGRPVDCMAIGVIM-YILSGNPPFYEEVEDDYENHDKULFRKTLAGDYEDSPYWD 254
DB 11 RYGRPVDCMAIGVIM-YILSGNPPFYEEVEDDYENHDKULFRKTLAGDYEDSPYWD 70
QY 255 ISQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGVCAQIEKNFARAKK 314
DB 71 ISQAADLVTRLMVEODORTIAEBAISHEMIISGNAASDKNIKQGVCAQIEKNFARAKK 130
QY 315 KAVVTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAASGATAPSGADAPAA 374
DB 131 KAVVTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAASGATAPSGADAPAA 190
QY 375 KSDNVAPADRSATPATDGSATPATDGSITPATDGSITPATDGSVTPVTRDSATPATDGRA 434
DB 191 KSDNVAPADRSATPATDGSATPATDGSITPATDGSITPATDGSVTPVTRDSATPATDGRA 250
QY 435 TPATBESVTPPTQSSAMLATKAAATPEPMAOPDSTAPBEGATQAPSSKGEBAAGYAQ 494
DB 251 TPATBESVTPPTQSSAMLATKAAATPEPMAOPDSTAPBEGATQAPSSKGEBAAGYAQ 310
QY 495 SORREAS 501
DB 311 SORREAS 317

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RESULT 11
 US-09-764-875-725
 ; Sequence 725, Application US/09764875
 ; Publication No. US20040018969A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT202
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 725
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (197)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-725

Query Match 37.4%; Score 966; DB 11; Length 204;
Best Local Similarity 98.4%; Pred. No. 1.8e-55;
Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 186 YLAEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
DB 246 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
QY 306 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 365
DB 134 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 193
QY 366 PEGDAPAAK 375
DB 194 PEGDAPAAK 203

RESULT 12
US-09-764-868-832
Sequence 832, Application US/09764868
Patent No. US2002016871A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 832
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-832

Query Match 33.0%; Score 852; DB 9; Length 219;

Best Local Similarity 72.6%; Pred. No. 5.4e-48;
Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;
QY 186 YLAEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
DB 246 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
QY 306 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 365
DB 134 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 178
QY 366 PEGDAPAAKSDNVAPADRSATPATDGSATPATDGSATPATD-----GSITPA 413
DB 179 -----ADRKCPQPOQWEPVPPQPLMAVSPQPMEMASXQPLMGSVTPA 219

RESULT 13
US-09-764-875-1035
Sequence 1035, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT202
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1035
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1035

Query Match 33.0%; Score 852; DB 11; Length 219;
Best Local Similarity 72.6%; Pred. No. 5.4e-48;
Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;

QY 186 YLAEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGROGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
DB 246 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPYWDISQAADLVTRLMEVEQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
QY 306 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 365
DB 134 KNFAPAKKKAVRTTLMKRLRAPEQSTAAQASATDTATPGAGGATAAASGATSA 178
QY 366 PEGDAPAAKSDNVAPADRSATPATDGSATPATDGSATPATD-----GSITPA 413
DB 179 -----ADRKCPQPOQWEPVPPQPLMAVSPQPMEMASXQPLMGSVTPA 219

RESULT 14
US-09-817-181-4
Sequence 4, Application US/09817181
Patent No. US20020142427A1
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001189
CURRENT APPLICATION NUMBER: US/09/817,181
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 370
TYPE: PRS
ORGANISM: Human
US-09-817-181-4

Query Match 30.7%; Score 793; DB 9; Length 370;
Best Local Similarity 43.7%; Pred. No. 7, 4e-44;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YNPSSEVTDVYDGVYKTEEFCEIFRAKDTGKLTCKKFKQKRGKRRKAAKEIGI 73
DB 10 WKQAEIDRIDYDFRDVLTGAFSEVILAEKRTQKLVAKICKALEGKESGMEIEIAV 69
QY 74 LKQVGHENILQVDVFNTRKEVFIFLELATGREVFMIDOGYSEBRTSNVROYLEAV 133
DB 70 LHKIKHPNIVALLDDIYESGHLTYLIMQVSGELFDRIVEKGFYTERDASRLIFQVLDAY 129
QY 134 AYLSHSLIVRNKLENTLVYNNRLKNSKIIVSDPHLAKLEN--GLIKPCGTPBYLAPEV 191
DB 130 KYLHDLGIVHRDLKPENLIIYSLEDESKIMISDFGLSKNEDPGSVLSTACGTPGYVAPEV 189
QY 192 VGRQRYRPVDCVAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKRLIAGDYEPDSPY 251
DB 190 LQKPYSKAVDCWSIGVIAYIILCGYPPFYDE-----NDAKLFEQILKAEYEPDSPY 241
QY 252 WDDISQAADLVTRLMVEVDQRTAEALSHWISGNAASDKNTKQGYCAQIEKNPAPA 311
DB 242 WDDISQASDFTRLMEKDPKPKFTCEQALQHPMTIAGDTALDKNTHQSEYSEQIKKNPAKS 301
QY 312 KMKKAVRVTTLMKRLAPE--QSTAAQASATDTATPGAGCATTAAGAATAP 366
DB 302 KMKQAFNATVAVRMKRLQLTGTSQEGQGTASHGELLTPVAGGPAAGCCCRDCCVP 358

RESULT 15
US-09-769-970-19
Sequence 19, Application US/09769970
Publication No. US20030170219A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Corley, Neil G.
Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Puri
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 790790
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-769-970-19

Query Match 30.7%; Score 793; DB 10; Length 370;
Best Local Similarity 43.7%; Pred. No. 7, 4e-44;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YNPSSEVTDVYDGVYKTEEFCEIFRAKDTGKLTCKKFKQKRGKRRKAAKEIGI 73
DB 10 WKQAEIDRIDYDFRDVLTGAFSEVILAEKRTQKLVAKICKALEGKESGMEIEIAV 69
QY 74 LKQVGHENILQVDVFNTRKEVFIFLELATGREVFMIDOGYSEBRTSNVROYLEAV 133
DB 70 LHKIKHPNIVALLDDIYESGHLTYLIMQVSGELFDRIVEKGFYTERDASRLIFQVLDAY 129
QY 134 AYLSHSLIVRNKLENTLVYNNRLKNSKIIVSDPHLAKLEN--GLIKPCGTPBYLAPEV 191
DB 130 KYLHDLGIVHRDLKPENLIIYSLEDESKIMISDFGLSKNEDPGSVLSTACGTPGYVAPEV 189
QY 192 VGRQRYRPVDCVAIGVIMYILLSGNPPFYEEVEEDDYENHDKNLFKRLIAGDYEPDSPY 251
DB 190 LQKPYSKAVDCWSIGVIAYIILCGYPPFYDE-----NDAKLFEQILKAEYEPDSPY 241
QY 252 WDDISQAADLVTRLMVEVDQRTAEALSHWISGNAASDKNTKQGYCAQIEKNPAPA 311
DB 242 WDDISQASDFTRLMEKDPKPKFTCEQALQHPMTIAGDTALDKNTHQSEYSEQIKKNPAKS 301
QY 312 KMKKAVRVTTLMKRLAPE--QSTAAQASATDTATPGAGCATTAAGAATAP 366
DB 302 KMKQAFNATVAVRMKRLQLTGTSQEGQGTASHGELLTPVAGGPAAGCCCRDCCVP 358

Search completed: April 23, 2004, 15:55:38
Job time : 50 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2004, 15:47:09 ; Search time 23 Seconds

(without alignments)
1124.548 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581

Sequence: 1 MPFGCVTLGDKKNVQPSSEV.....SSKGEFAGYAGSQRERAS 501

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/6CTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2581	100.0	501	US-09-734-030-2	Sequence 2, Appl1
2	2581	100.0	501	US-10-153-921-2	Sequence 2, Appl1
3	793	30.7	370	US-08-878-989-19	Sequence 19, Appl1
4	793	30.7	370	US-09-272-796-19	Sequence 19, Appl1
5	793	30.7	370	US-09-457-0408-31	Sequence 31, Appl1
6	767.5	29.7	385	US-09-733-388-2	Sequence 2, Appl1
7	764	29.6	355	US-09-579-664B-10	Sequence 10, Appl1
8	754.5	29.2	356	US-09-733-388-4	Sequence 4, Appl1
9	715	27.7	358	US-09-230-896C-29	Sequence 4, Appl1
10	642.5	24.9	343	US-08-878-989-5	Sequence 5, Appl1
11	642.5	24.9	343	US-08-272-796-5	Sequence 5, Appl1
12	589.5	22.8	424	US-08-715-568A-1	Sequence 1, Appl1
13	580.5	22.5	765	US-09-975-326-4	Sequence 4, Appl1
14	580.5	22.5	765	US-10-217-357-4	Sequence 4, Appl1
15	580.5	22.5	766	US-09-975-326-2	Sequence 2, Appl1
16	580.5	22.5	766	US-10-217-357-2	Sequence 2, Appl1
17	565.5	21.9	565	US-09-800-960-2	Sequence 2, Appl1
18	565.5	21.9	565	US-10-096-960-2	Sequence 2, Appl1
19	546	21.2	566	US-07-857-224B-24	Sequence 24, Appl1
20	535	20.7	556	US-09-800-960-4	Sequence 4, Appl1
21	535	20.7	556	US-10-096-960-4	Sequence 4, Appl1
22	504	19.5	264	US-07-857-224B-18	Sequence 18, Appl1
23	490	19.0	264	US-07-857-224B-19	Sequence 19, Appl1
24	489.5	19.0	295	US-07-951-715A-23	Sequence 23, Appl1
25	489.5	19.0	295	US-08-459-448A-23	Sequence 23, Appl1
26	489.5	19.0	295	US-08-459-595A-23	Sequence 23, Appl1
27	489.5	19.0	295	US-08-459-504B-23	Sequence 23, Appl1

28	489.5	19.0	295	US-08-459-444-23	Sequence 23, Appl1
29	489.5	19.0	295	US-09-547-432-23	Sequence 23, Appl1
30	483.5	18.7	331	US-08-810-712-24	Sequence 24, Appl1
31	483.5	18.7	1423	US-08-810-712-10	Sequence 10, Appl1
32	480.5	18.6	514	US-09-841-683-2	Sequence 2, Appl1
33	468.5	18.2	817	US-09-992-481-4	Sequence 4, Appl1
34	467	18.1	387	US-08-713-828-3	Sequence 3, Appl1
35	467	18.1	387	US-08-919-627-3	Sequence 3, Appl1
36	467	18.1	387	US-09-096-245-3	Sequence 3, Appl1
37	467	18.1	387	US-09-457-040B-30	Sequence 30, Appl1
38	460	17.8	454	US-09-159-385-1	Sequence 1, Appl1
39	460	17.8	454	US-09-186-277-1	Sequence 1, Appl1
40	459.5	17.8	388	US-08-713-828-5	Sequence 5, Appl1
41	459.5	17.8	388	US-08-919-627-5	Sequence 5, Appl1
42	459.5	17.8	388	US-09-096-245-5	Sequence 5, Appl1
43	457	17.7	388	US-08-713-828-4	Sequence 4, Appl1
44	457	17.7	388	US-08-919-627-4	Sequence 4, Appl1
45	457	17.7	388	US-09-096-245-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1					
US-09-734-030-2					
Sequence 2, Application US/09734030					
Patent No. 6461846					
GENERAL INFORMATION:					
APPLICANT: BEASLEY, Ellen M.					
APPLICANT: MERKLOV, Gennady					
APPLICANT: KETCHUM, Karen A.					
APPLICANT: WEI, Ming-Hui					
APPLICANT: DIPRANCESCO, Valentina					
APPLICANT: YAN, Chunhua					
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC					
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES					
TITLE OF INVENTION: THERMOP					
FILE REFERENCE: CL000612					
CURRENT APPLICATION NUMBER: US/09/734,030					
CURRENT FILING DATE: 2000-12-12					
PRIOR APPLICATION NUMBER: 60/207,261					
PRIOR FILING DATE: 2000-05-30					
NUMBER OF SEQ ID NOS: 3					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 2					
LENGTH: 501					
TYPE: PRT					
ORGANISM: HUMAN					
US-09-734-030-2					
Query Match					
Best Local Similarity 100.0%; Pred. No. 4.1e-180;					
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MPFGCVTLGDKKNVQPSSEVTRDYDLGOVITKEEFCETFRADKKTGKLTCKFKQKEDG	60		
DB	1	MPFGCVTLGDKKNVQPSSEVTRDYDLGOVITKEEFCETFRADKKTGKLTCKFKQKEDG	60		
QY	61	RKVRKAANEIGILKXVXHPNLIQVDFVTRKEYFIFLELATGREVFDMIDQYSEER	120		
DB	61	RKVRKAANEIGILKXVXHPNLIQVDFVTRKEYFIFLELATGREVFDMIDQYSEER	120		
QY	121	DSNVVROVLEAVATLSIKTYHRNLKLENNVYVYRNLKNSKIVISDFILAKLENLKEP	180		
DB	121	DSNVVROVLEAVATLSIKTYHRNLKLENNVYVYRNLKNSKIVISDFILAKLENLKEP	180		
QY	181	CGTPEVLAPEVVGRRYGRPVDCNAIGVIMYILISGNPFYEEVEDDYENHDKLFRKI	240		
DB	181	CGTPEVLAPEVVGRRYGRPVDCNAIGVIMYILISGNPFYEEVEDDYENHDKLFRKI	240		
QY	241	LAGDYEFDSFYDDISQAKDLYTSLMEVEVDORITAEASISHEWISGNASDKNITKQGV	300		
DB	241	LAGDYEFDSFYDDISQAKDLYTSLMEVEVDORITAEASISHEWISGNASDKNITKQGV	300		

Thu Apr 29 08:44:18 2004

us-10-669-689-2.ra1

Page 2

[illegible]

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RESULT 2
US-10-153-921-2
; Sequence 2, Application US/10153921
; Patent No. 665316
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO0612D1V
; CURRENT APPLICATION NUMBER: US/10/153,921
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/207,261
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-10-153-921-2

```

Query March	100.0%;	Score 2581;	DB 4;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 4,1e-180;		
Matches 501; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MEFGCVTLDDKKNYNQPSVETDRYDLGVKITEEFCETFRAXDXTTKLHTCKKQFRDG	60
Dp	1	MEFGCVTLDDKKNYNQPSVETDRYDLGVKITEEFCETFRAXDXTTKLHTCKKQFRDG	60
QY	61	RKTRKAANEIGILKMWKHPNLTQVDVFTRKEXFIFLELATGREVFDMLDQYYSER	120
Dp	61	RKTRKAANEIGILKMWKHPNLTQVDVFTRKEXFIFLELATGREVFDMLDQYYSER	120
QY	121	DTSNVVRQVLEAVAYHLSKIVHRNKLKEMLYYVYRLLNSKXIVSDHLAKLENGLIKEP	180
Dp	121	DTSNVVRQVLEAVAYHLSKIVHRNKLKEMLYYVYRLLNSKXIVSDHLAKLENGLIKEP	180
QY	181	CGPEYLAEEVNGRQYRGPRVDCMALGIYIMTLLSGNPPFEEVEEDDYENHDKNLPKRI	240
Dp	181	CGPEYLAEEVNGRQYRGPRVDCMALGIYIMTLLSGNPPFEEVEEDDYENHDKNLPKRI	240
QY	241	IAGDYEFDSPPYMDDISQAOKDLVTFLMEVEDORTLEBAASHWISIGNAASDKNIXDGV	300
Dp	241	IAGDYEFDSPPYMDDISQAOKDLVTFLMEVEDORTLEBAASHWISIGNAASDKNIXDGV	300
QY	301	CAQIEKNPFAKMKKAVRTTLMKRLRPAEOSTTAAQOSASATTPAGAAGGTTAAAS	360
Dp	301	CAQIEKNPFAKMKKAVRTTLMKRLRPAEOSTTAAQOSASATTPAGAAGGTTAAAS	360
QY	361	GATSAPEGGAARAAKSDNVAPADRSGATPATDGSATPATDGSVTPATDGSITPATDGSVP	420
Dp	361	GATSAPEGGAARAAKSDNVAPADRSGATPATDGSATPATDGSVTPATDGSITPATDGSVP	420

[illegible]

RESULT 3
US-08-878-989-19
; Sequence 19, Application US/08878989

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Guegler, Karl G.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

NUMBER OF SEQUENCES: 21

ADDRESSEE: Incyte Pharmaceuticals, Inc.

CITY: Palo Alto

COUNTRY: USA

COMPUTER READAB ;

COMPUTER: IBM Compat

```
SOFTWARE: FastSeq for Windows Version 2.0.0
```

APPLICATION NUMBER: US/08/878,989

CLASSIFICATION: 435

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,749

TELECOMMUNICATION INFORMATION:

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 19:

LENGTH: 370 amino acids

STRANDEDNESS: single

IMMEDIATE SOURCE:

CLONE: 790790

US-08-878-989-19

Query Match 30.7%; Score 793; DB 2; Length 370;

Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3

14 YNQPSEVTRDYDLGQVIKTEEFCEIFRAKDKTTGKLTCKKFQKRDRGRVKRAKNEIGI 73

Db 10 WKQAEIDRIDYDFRDVLGTGAFSEVILAEADKRTQKLVAIKIAKEALEGKEGSMENIAY 69

74 LKMKHPNIIQLVDVFVTRKEYFIFLEIATGREVEDWILDQGYSERDTSNVVRQVLEAV 133

Db 70 LHKIKHPNIVALDDIYESGGHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDVAV 129
QY 134 AYHSLKTVHRNLTENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
Db 130 KYLHDLGIVHRDLKPEMLLYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTPGVAPAEV 189
QY 192 VGRQRYGRPVDCMAIGVIMYLLSGNPFEEVEEDDYENHDKLFRKILLAGDYEFDSPY 251
Db 190 LAQKPYSAVDCCMSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
QY 252 WDISQAAXDLVTRLMVEYQDQRTAEBAISHEMIISGNASADKNIKDGVCQAIENKFPARA 311
Db 242 WDISDSAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAPS 301
QY 312 KWKAQAVRVTTLMKRLRAPE--QSTTAAQASATDTATPGAGATPAAASGATSAP 366
Db 302 KWKAQAFNATAVVRHMRKLQIGTSQEGGQTASHGELLTPVAGGPAGCCCRDCCVPEP 358

RESULT 4
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Puryl
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
US-09-272-796-19
Query Match 30.7%; Score 793; DB 3; Length 370;

Best Local Similarity 43.7%; Pred. No. 4.3e-50;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;
QY 14 YNPSSEVTDRLDQGVITKEEFCIFRAKDKTTGKLTCKKFORRDKVRKAAKEIGI 73
Db 10 WKQADIRIDIVDFPDVLTGTAFASEVILAEDEKRTQKLVAKICIAEALGKESGSENEIAY 69
QY 74 LKMKVHNILQVDFVTRKKEVFFLELATREVDWILDDGYISEEDTSNVVQVLEAV 133
Db 70 LHKIKHPNIVALDDIYESGGHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDVAV 129
QY 134 AYHSLKTVHRNLTENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
Db 130 KYLHDLGIVHRDLKPEMLLYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTPGVAPAEV 189
QY 192 VGRQRYGRPVDCMAIGVIMYLLSGNPFEEVEEDDYENHDKLFRKILLAGDYEFDSPY 251
Db 190 LAQKPYSAVDCCMSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
QY 252 WDISQAAXDLVTRLMVEYQDQRTAEBAISHEMIISGNASADKNIKDGVCQAIENKFPARA 311
Db 242 WDISDSAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAPS 301
QY 312 KWKAQAVRVTTLMKRLRAPE--QSTTAAQASATDTATPGAGATPAAASGATSAP 366
Db 302 KWKAQAFNATAVVRHMRKLQIGTSQEGGQTASHGELLTPVAGGPAGCCCRDCCVPEP 358

RESULT 5
US-09-457-040B-31
; Sequence 31, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-457-040B-31
Query Match 30.7%; Score 793; DB 4; Length 370;
Best Local Similarity 43.7%; Pred. No. 4.3e-50;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;
QY 14 YNPSSEVTDRLDQGVITKEEFCIFRAKDKTTGKLTCKKFORRDKVRKAAKEIGI 73
Db 10 WKQADIRIDIVDFPDVLTGTAFASEVILAEDEKRTQKLVAKICIAEALGKESGSENEIAY 69
QY 74 LKMKVHNILQVDFVTRKKEVFFLELATREVDWILDDGYISEEDTSNVVQVLEAV 133
Db 70 LHKIKHPNIVALDDIYESGGHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDVAV 129
QY 134 AYHSLKTVHRNLTENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
Db 130 KYLHDLGIVHRDLKPEMLLYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTPGVAPAEV 189
QY 192 VGRQRYGRPVDCMAIGVIMYLLSGNPFEEVEEDDYENHDKLFRKILLAGDYEFDSPY 251
Db 190 LAQKPYSAVDCCMSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
QY 252 WDISQAAXDLVTRLMVEYQDQRTAEBAISHEMIISGNASADKNIKDGVCQAIENKFPARA 311
Db 242 WDISDSAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAPS 301
QY 312 KWKAQAVRVTTLMKRLRAPE--QSTTAAQASATDTATPGAGATPAAASGATSAP 366
Db 302 KWKAQAFNATAVVRHMRKLQIGTSQEGGQTASHGELLTPVAGGPAGCCCRDCCVPEP 358

Db 302 KKQAFNATAVVRHNRKQLGTSQSGOGTASHGHEILTPVAGGPAAGCCCPDCCVP 358

RESULT 6
US-09-733-388-2

Sequence 2, Application US/09733388

Patent No. 6602698

GENERAL INFORMATION:

APPLICANT: Donoho, Greg

APPLICANT: Scoville, John

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Friedrich, Glenn

APPLICANT: Zambrowicz, Brian

APPLICANT: Abulin, Alejandro

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0103-USA

CURRENT APPLICATION NUMBER: US/09/733.388

PRIOR FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,428

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 385

TYPE: PRT

ORGANISM: Homo sapiens

US-09-733-388-2

Query Match 29.7%; Score 767.5; DB 4; Length 385;

Best Local Similarity 40.4%; Pred. No. 3.3e-48;

Matches 152; Conservative 79; Mismatches 122; Indels 23; Gaps 5;

16 QPSEVTDRLDGVITKEEFCEIFRAKDTTGLKHTCKKQKRDGRKVRKAANEIGILK 75

15 QAEIDIKIPEFKETLTGTGAFSEVTLAEKATGKLPFAVKCIPKALKGKSSIEINEIAVL 74

76 MKHGPNILOLVDFVTRKKEFFLELATGREVFDMILDOGYSEBDTSNVVQVLEAVAY 135

75 KIKHENIVALIEDIYESPNHLVLMQVSGELFDRIVEKGFTEKXASTLIRQVLDVAYY 134

136 LHSKIVHNLKLENIYVTRNLKNSKIYSDPHLAKLS--NGLIKPQCGTPRYLAEVVG 193

135 LHRMGIVHDLKPEENILYISODESKIMISDFGLSMEKSGVMTACGTPGVAAPEVLA 194

194 RQRYGRPYDOWAIGVIMYITLLSGNPFVEEVEDDENHDKNLFKRILAGDYEPDSPYMD 253

195 QKYSKAVDOWMSIGVIAIYLLCGYPPFYDE-----NDSKLPQILKAEYEPDSPYMD 246

254 DISQAAKDLVTRIMEVEDQRTTAERAISEWISGNAASDKNIKQGVCAQIEKNFARAKW 313

247 DISDSAKDPIRLNMEKDPNKRYTCEQAAHPWLAGDTALNKNIHESVSAQIRKNFAKSKW 306

314 KXAVRTTLMKRLR-----APEGSSTAAGS-----ASADITNTPGA-----AGCATAAAS 360

307 RQAFNATAVVRHNRKQLGTSQSGOGTASHGHEILTPVAGGPAAGCCCPDCCVP 366

361 GATSAPEGDAARAKS 376

367 GAERRRPPTTVTAVHS 382

Db 302 KKQAFNATAVVRHNRKQLGTSQSGOGTASHGHEILTPVAGGPAAGCCCPDCCVP 358

RESULT 7

US-09-579-664B-10

Sequence 10, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Bird, Timothy A.

APPLICANT: Virca, G. Duke

APPLICANT: Martin, Unja

APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REFERENCE: 2923-A

CURRENT APPLICATION NUMBER: US/09/579,664B

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10

LENGTH: 355

TYPE: PRT

ORGANISM: Mus musculus

US-09-579-664B-10

Query Match 29.6%; Score 764; DB 4; Length 355;

Best Local Similarity 43.0%; Pred. No. 5.3e-48;

Matches 142; Conservative 78; Mismatches 100; Indels 10; Gaps 2;

16 QPSEVTDRLDGVITKEEFCEIFRAKDTTGLKHTCKKQKRDGRKVRKAANEIGILK 75

15 QAEIDIKIPEFKETLTGTGAFSEVTLAEKATGKLPFAVKCIPKALKGKSSIEINEIAVL 74

76 MKHGPNILOLVDFVTRKKEFFLELATGREVFDMILDOGYSEBDTSNVVQVLEAVAY 135

75 KIKHENIVALIEDIYESPNHLVLMQVSGELFDRIVEKGFTEKXASTLIRQVLDVAYY 134

136 LHSKIVHNLKLENIYVTRNLKNSKIYSDPHLAKLS--NGLIKPQCGTPRYLAEVVG 193

135 LHRMGIVHDLKPEENILYISODESKIMISDFGLSMEKSGVMTACGTPGVAAPEVLA 194

194 RQRYGRPYDOWAIGVIMYITLLSGNPFVEEVEDDENHDKNLFKRILAGDYEPDSPYMD 253

195 QKYSKAVDOWMSIGVIAIYLLCGYPPFYDE-----NDSKLPQILKAEYEPDSPYMD 246

254 DISQAAKDLVTRIMEVEDQRTTAERAISEWISGNAASDKNIKQGVCAQIEKNFARAKW 313

247 DISDSAKDPIRLNMEKDPNKRYTCEQAAHPWLAGDTALNKNIHESVSAQIRKNFAKSKW 306

314 KXAVRTTLMKRLR-----APEGSSTAAGS-----ASADITNTPGA-----AGCATAAAS 360

307 RQAFNATAVVRHNRKQLGTSQSGOGTASHGHEILTPVAGGPAAGCCCPDCCVP 366

16 QPSEVTDRLDGVITKEEFCEIFRAKDTTGLKHTCKKQKRDGRKVRKAANEIGILK 75

RESULT 8

US-09-733-388-4

Sequence 4, Application US/09733388

Patent No. 6602698

GENERAL INFORMATION:

APPLICANT: Donoho, Greg

APPLICANT: Scoville, John

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Friedrich, Glenn

APPLICANT: Zambrowicz, Brian

APPLICANT: Abulin, Alejandro

TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0103-USA

CURRENT APPLICATION NUMBER: US/09/733.388

PRIOR FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,428

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 356

TYPE: PRT

ORGANISM: Homo sapiens

US-09-733-388-4

Query Match 29.2%; Score 754.5; DB 4; Length 356;

Best Local Similarity 40.1%; Pred. No. 2.6e-47;

Matches 147; Conservative 84; Mismatches 109; Indels 27; Gaps 4;

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Db      15 QAEIDIKKIFEEKELTGAFSEVVLAAEKAIGKLFVAKCIPKALKKKESSINENIAVLR 74
QY      76 MYKPNILQADVVTREKREYIFLELATGREVPMILDOGYSERDTSNVVRQVLEAVAY 135
Db      75 KIKHENVIALEDIESPNHLVYVQVYSGELFPRIVKGFYTKDASTIIRQVLDVAVY 134
QY      136 LHSIKIVHRNKLKLENLYVYVNLKNSKIVISDFHLAKLE--NGLIKECGTPEYLAEVVG 193
Db      135 LHRMGIVHRDLKPNLKYSGDESKIMISDFGLSKKEGKQDVSTACGPGVYAEPLVA 194
QY      194 KQRPGRPVDCALIGVIMTILISGNPFYEEVEEDYENHDKNLFKRLIADYEPDSPYWD 253
Db      195 QKPYSKAVDCMSIGIVAYIILCGYPPFYDE-----NDSKLFEEQILKAKEYEFDSPYWD 246
QY      254 DISQAADLVYRLMEVODORTAEALISHENISGNAASDXTKDYCAQIENKPARAKY 313
Db      247 DISQAADLVYRLMEVODORTAEALISHENISGNAASDXTKDYCAQIENKPARAKY 305
QY      314 KKAIVYTTIMKRLRAPQSGSTAAQASATDTATPGAAGATATAAAGATSAEGDARA 373
Db      306 KQAFNATAVYVHRKRLHGLSSLDSSNMS-----VSSSLASQKDCAYV 349
QY      374 AKSDNVA 380
Db      350 AKPESL 356

```

RESULT 9
US-09-230-896C-29
Sequence 29, Application US/09230896C
Patent No. 6635479
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Hypochlamys-Specific Polypeptides
FILE REFERENCE: TSRI-548.1
CURRENT APPLICATION NUMBER: US/09/230,896C
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: 60/023,220
PRIOR FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 358
TYPE: PRT
ORGANISM: ratus ratus
US-09-230-896C-29

Query Match 27.7%; Score 715; DB 4; Length 358;
Best Local Similarity 42.3%; Pred. No. 2e-44;
Matches 142; Conservative 72; Mismatches 112; Indels 10; Gaps 3;

```

QY      16 QPSEVTRDYDGOVYKTEEFCEIFRAKDXTGKLTCKKQKRGKRVKRAKNEIGILK 75
Db      7 QTEDISSVYEIREKLGSAFSEVVLAAQERGAHLVAKCIPKALKRGEALVENEIAVLR 66
QY      76 MYKPNILQADVVTREKREYIFLELATGREVPMILDOGYSERDTSNVVRQVLEAVAY 135
Db      67 RISHPNIALEDVYESHLYLAMELVYTGELFPRIMERGSYTKDASHLVGVYLGAVSY 126
QY      136 LHSIKIVHRNKLKLENLYVYVNLKNSKIVISDFHLAKLENG-LIKEPGTPEYLAEVVG 194
Db      127 LHSIGIVHRDLKPNLKYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTGYVAPELLEQ 186
QY      195 QKRPGRPVDCALIGVIMTILISGNPFYEEVEEDYENHDKNLFKRLIADYEPDSPYWD 254
Db      187 KPYKRAVDVWALGVISYILLCGYPPFYDE-----SDPELFQILRASVEYFDSPPWMD 238
QY      255 ISOAKLVYRLMEVODORTAEALISHENISGNAASDKNIKQGVCAQIEKNPARAKY 314
Db      239 ISBAKQVIRHLRDLKPNLKYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTGYVAPELLEQ 298

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QY      315 KKAIVYTTIMKRLRAPQSGSTAAQASATDTATPG 349
Db      299 RAFNATSFRLHRIKLGQSPGEGBEASRQGMTRSHSG 334

```

RESULT 10
US-08-878-989-5
Sequence 5, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
TITLE OF INVENTION: KINASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STANDARDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-08-878-989-5

Query Match 24.9%; Score 642.5; DB 2; Length 343;
Best Local Similarity 40.6%; Pred. No. 3.6e-39;
Matches 126; Conservative 69; Mismatches 106; Indels 9; Gaps 2;

```

QY      19 EYTDYRDYDGOVYKTEEFCEIFRAKDXTGKLTCKKQKRGKRVKRAKNEIGILK 78
Db      10 DISSVYERIRERGSAGFSEVVLAAQERGAHLVAKCIPKALKRGEALVENEIAVLR 69
QY      79 HNNILQADVVTREKREYIFLELATGREVPMILDOGYSERDTSNVVRQVLEAVAYLHS 138
Db      70 HNNIIVALEDVHESPHLYLAMELVYTGELFPRIMERGSYTKDASHLVGVYLGAVSYLHS 129
QY      139 LKIVHRNKLKLENLYVYVNLKNSKIVISDFHLAKLENG-LIKEPGTPEYLAEVVGGRORY 197
Db      130 LGIIVHRDLKPNLKYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTGYVAPELLEQKPY 189

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US-09-975-326-2
; Sequence 2, Application US/09975326
; Patent No. 6476210
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mabur, Brian
; TITLE OF INVENTION: No. 6476210e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0254-USA
; CURRENT APPLICATION NUMBER: US/09/975,326
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,821
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-975-326-2

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Query Match      22.5%; Score 580.5; DB 4; Length 766;
Best Local Similarity 30.3%; Pred. No. 3,3e-34;
Matches 146; Conservative 72; Mismatches 151; Indels 113; Gaps 10;

QY 15 NOPSEVTDYDIDGQVITEFCEIFRAKDKTGLTKLTCCKFQKRDGRVRAKAKNEIGIL 74
DB 385 SESSTLEKXKIGKVIKGDNFVAVKECIDRSTGEFALKIIDKACGCKEHLIENEVSIL 444
QY 75 KAVKAPNIIQVDFVTRKEYRIFLELATGREVFMILDQGYSERDTSNRYQVLEAVA 134
DB 445 RRYKHPNIIIMLVEMETATELFLVMELVGGLFDALTSSTKYTERDGSAMVYNLANLR 504
QY 135 YLHSLKIVHRNKLKENTLV---YNNRLKNSKIVISDPHLAKLGNLIXEPCGFPEYLAPEV 191
DB 505 YLHGSLIVHRDIPENLVCEYPDGTSKAK--LGDGLATVVEGFLPYVCGIPYVAPET 562
QY 192 VGRQRYGRPEVDCMAIGVIVYIILSGNPPYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 251
DB 563 IAEITGGLKVDIMAGVITYIILCGFPFRSE-----NNLGEDLFDQILAGKLEFPAPY 616
QY 252 WDDISQAADLVTRLMVEZODORTIAEAIISHEWISGNAPSDKNITKGYCAQIEKNFAPA 311
DB 617 WDIITDSAKELISQMLQVWVEARCTAGQIISHPWVSDDASQENNMQAQEVYTKLKHFNNA 676
QY 312 KMKKAVRVTITMKRLAPRQSSPAQAQSA---SATDTATPGAAGATATAAAGATSAPEG 368
DB 677 -----LPRKONSTTGVSIVKNTALD-----KEG 699
QY 369 DABAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTPVTRSATP 428
DB 700 QT-----FCSKHQDSGRFGME-----PISPY----- 721
QY 429 ATDGRAIPATESSTVPTTOSAMLAATKAATPEPANAQPDSTAPEGATQAPSSKGEZA 488
DB 722 -----PPSVVE-----IPVGEAVPAPTPPESPTPHCPAPAPGGER 757
QY 489 AG 490
DB 758 AG 759

```

Search completed: April 23, 2004, 15:50:50
Job time : 25 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: April 23, 2004, 15:43:58 ; Search time 59 Seconds
(without alignments)
2399.259 Million cell updates/sec

Title: US-10-669-689-2
Perfect score: 2581
Sequence: 1 MPRGCTLTDBKKNYNQPSFV.....SSKGEPAAGYAGSQGREAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_2904n04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2581	100.0	501	5	AAM48279 Human pro
2	2577	99.8	501	4	AAE11783 Human kin
3	2566	99.4	501	4	AAM38988 Human pol
4	2566	99.4	501	4	AAG67539 Amino aci
5	2563	99.3	501	4	AAM93379 Human pol
6	2403	93.1	473	4	ABU52788 Human sig
7	2402.5	93.1	470	4	AAM93404 Human pol
8	2402.5	93.1	470	4	AAB20327 Human pro
9	2398.5	92.9	470	4	AAM93679 Human pol
10	2391.5	92.7	470	4	AAM89887 Human pol
11	1403.5	54.4	284	3	AAB42348 Human ORF
12	1255.5	48.6	289	4	ABU52789 Human sig
13	978	37.9	187	4	ABU52790 Human sig
14	966	37.4	204	4	AABU8207 Novel cen
15	852	33.0	219	4	AABU1267 Novel sig
16	852	33.0	219	4	AABU8517 Novel cen
17	852	33.0	219	7	ADB93975 Human nov
18	793	30.7	370	6	AAE34492 Human cam
19	775	29.9	332	7	ADC15044 Calcium/c
20	771	29.9	317	5	ABG69794 Human kin
21	771	29.9	357	4	AAE11768 Human kin
22	767.5	29.7	385	4	AAM34482 Human pol
23	767.5	29.7	385	4	AAE84359 Amino aci
24	766	29.7	357	4	AAU03508 Human pro
25	764	29.6	355	4	AAB50055 Murine De

26	764	29.6	355	4	AAE11777 Human kin
27	764	29.6	355	4	AAM41268 Human pol
28	764	29.6	355	5	ABO08178 Human cam
29	754.5	29.2	356	4	AAE84360 Amino aci
30	748.5	29.0	389	3	AAE68793 Amino aci
31	748.5	29.0	405	4	ABE58176 Drosophil
32	747.5	29.0	476	5	AAE22764 Human cal
33	747.5	29.0	476	5	ABG69793 Human CAD
34	747.5	29.0	476	7	AAE56391 Human pro
35	747.5	29.0	476	7	AAE56387 Human pro
36	747.5	29.0	476	7	ADD45328 Human pro
37	747.5	29.0	497	4	AAE41547 Human pol
38	746	28.9	460	5	ABG69792 Human CAD
39	738	28.6	567	4	AAE39761 Human pol
40	727.5	28.2	503	4	ABG05970 Novel hum
41	720	27.9	309	7	AAE56389 Rat Prote
42	720	27.9	309	7	ADD45326 Rat Prote
43	720	27.9	309	7	AAE56385 Rat Prote
44	720	27.9	309	7	ADD46031 Rat Prote
45	718	27.6	326	6	AAE32426 Human kin

ALIGNMENTS

RESULT 1
ID AAM48279 standard; protein: 501 AA.
AC AAM48279;
DT 03-APR-2002 (first entry)
DE Human protein kinase.
KW Human; protein kinase; enzyme; brain; lung; hippocampus;
KW calmodulin-binding kinase; gene therapy.
XX
OS Homo sapiens.
PN WC0200192492-A2.
XX
PD 06-DEC-2001.
PF 30-MAY-2001; 2001MO-US017327.
XX
PR 30-MAY-2000; 2000US-0207281P.
XX
PR 12-DEC-2000; 2000US-00734030.
XX
XX (APPL-) APPLERA CORP.
XX Yan C, Wei M, Ketchum K, Merkulov G, Beasley EM;
XX WPI: 2002-097770/13.
XX N-PSDB; ABA95682.
XX
XX New calmodulin-binding kinase peptides and nucleic acid encoding the
XX peptide, useful as models for developing human therapeutic targets or in
XX screening for compounds that modulate kinase.
XX
XX Claim 1; fig 2; 75pp; English.
XX
XX The present sequence is the protein sequence for a human protein kinase.
XX The protein kinase coding sequence is expressed in the brain (both infant
XX and adult brain), lung and hippocampus. The protein kinase is related to
XX the calmodulin-binding kinase subfamily. The protein kinase and its
XX coding sequence can be used as models for the development of human
XX therapeutic targets, in the identification of therapeutic proteins, and
XX serve as targets for the development of human therapeutic agents that
XX modulate kinase activity in cells and tissues that express the kinase. In
XX addition, the protein kinase coding sequence can be used for treating a
XX disorder associated with nucleic acid expression of the kinase gene, in
XX particularly biological and pathological processes that are mediated by

Db 61 RYRKAANKNEIGILKRVKHPNIIQLVDVFTVTRKEYIFILELATGREVFWILDQGYSER 120

QY 121 DTSNVVROVLEAVAYLHSLKIVHRNLKLENYVYNNRLKNSKIYISDFHLAKLENGLKEP 180

Db 121 DTSNVVROVLEAVAYLHSLKIVHRNLKLENYVYNNRLKNSKIYISDFHLAKLENGLKEP 180

QY 181 CGTPEYLAPENVGRQYGRPVDCMAIGVIMYILLSGNPPFYEEVEDDYENHDKLFRKI 240

Db 181 CGTPEYLAPENVGRQYGRPVDCMAIGVIMYILLSGNPPFYEEVEDDYENHDKLFRKI 240

QY 241 LAGDYEPFSPYWDIDISQAKDLVTRLMVEVQDORITAEALISHEMIISGNAASDKNIKQGV 300

Db 241 LAGDYEPFSPYWDIDISQAKDLVTRLMVEVQDORITAEALISHEMIISGNAASDKNIKQGV 300

QY 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPBOSSTAAQASATDTTPAAGATTAAS 360

Db 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPBOSSTAAQASATDTTPAAGATTAAS 360

QY 361 GATSAPEGDAAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420

Db 361 GATSAPEGDAAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420

QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAQPDSTAPEGATGAP 480

Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAQPDSTAPEGATGAP 480

QY 481 PSSKGEBAAGYAQESQREBAS 501

Db 481 PSSKGEBAAGYAQESQREBAS 501

RESULT 3

AA038988 standard; protein; 501 AA.

AA038988;

22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 2133.

Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

Homo sapiens.

MO20015312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US034263.

23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-0048725.
25-APR-2000; 2000US-0052317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

Tang Y.T., Liu C., Aseundi V., Chen R., Ma Y., Qian X.B., Ren F., Wang D., Wang Z., Wehrman T., Xu C., Xue A.J., Yang Y., Zhang J., Zhao Q., Zhou F., Goodrich R., Drmanac R.T., WPI; 2001-442253/47.

DR N-PSDB; AA158144.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX

PS Example 4; SEQ ID NO 2133; 10078pp; English.

CC The invention relates to human nucleic acids (AA15798-AA161369) and the

CC encoded polypeptides (AA08642-AA42213) with noctropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localized neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX

SQ Sequence 501 AA;

Query Match

Best Local Similarity 99.4%; Score 2566; DB 4; Length 501;

Matches 498; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFGCVTLGDKKNYNQPSVETDRYDLQGVITKEBFCSIFRAKDTTGTCKKFORRG 60

Db 1 MPFGCVTLGDKKNYNQPSVETDRYDLQGVITKEBFCSIFRAKDTTGTCKKFORRG 60

QY 61 RYRKAANKNEIGILKRVKHPNIIQLVDVFTVTRKEYIFILELATGREVFWILDQGYSER 120

Db 61 RYRKAANKNEIGILKRVKHPNIIQLVDVFTVTRKEYIFILELATGREVFWILDQGYSER 120

QY 121 DTSNVVROVLEAVAYLHSLKIVHRNLKLENYVYNNRLKNSKIYISDFHLAKLENGLKEP 180

Db 121 DTSNVVROVLEAVAYLHSLKIVHRNLKLENYVYNNRLKNSKIYISDFHLAKLENGLKEP 180

QY 181 CGTPEYLAPENVGRQYGRPVDCMAIGVIMYILLSGNPPFYEEVEDDYENHDKLFRKI 240

Db 181 CGTPEYLAPENVGRQYGRPVDCMAIGVIMYILLSGNPPFYEEVEDDYENHDKLFRKI 240

QY 241 LAGDYEPFSPYWDIDISQAKDLVTRLMVEVQDORITAEALISHEMIISGNAASDKNIKQGV 300

Db 241 LAGDYEPFSPYWDIDISQAKDLVTRLMVEVQDORITAEALISHEMIISGNAASDKNIKQGV 300

QY 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPBOSSTAAQASATDTTPAAGATTAAS 360

Db 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPBOSSTAAQASATDTTPAAGATTAAS 360

QY 361 GATSAPEGDAAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420

Db 361 GATSAPEGDAAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420

QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAQPDSTAPEGATGAP 480

Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAQPDSTAPEGATGAP 480

QY 481 PSSKGEBAAGYAQESQREBAS 501

Db 481 PSSKGEBAAGYAQESQREBAS 501

RESULT 4

AA067539 standard; protein; 501 AA.

AA067539;

26-NOV-2001 (first entry)

XX	DE	Amino acid sequence of human kinase 2504.	
XX	KW	Human, kinase; 2504; 15977; 14760; cellular proliferative disorder;	
XX	KW	cellular differentiative disorder; neural disorder; immune disorder;	
XX	KW	cardiovascular disorder; liver disorder; skin disorder;	
XX	KW	skeletal muscle disorder; bone metabolism; cardiovascular disorder;	
XX	KW	viral disease; pain; metabolic disorder; blood vessel disorder;	
XX	KW	hepatic disorder; liver disorder.	
OS	XX	Homo sapiens.	
XX	XX		
XX	XX	Key	Location/Qualifiers
FT	FT	Modified-site	7..10
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	21..23
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Domain	24..286
FT	FT	Domain	/note= "serine/threonine kinase domain"
FT	FT	Domain	37..286
FT	FT	Domain	/note= "eukaryotic protein kinase domain"
FT	FT	Modified-site	46..48
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	51..53
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	59..62
FT	FT	Modified-site	/note= "predicted amidation site"
FT	FT	Modified-site	91..94
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	91..93
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	103..106
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	103..105
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	118..121
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	118..120
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	127..135
FT	FT	Modified-site	/note= "predicted tyrosine kinase phosphorylation site"
FT	FT	Modified-site	138..140
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	276..279
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	288..293
FT	FT	Modified-site	/note= "predicted N-myristoylation site"
FT	FT	Modified-site	292..294
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	341..344
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	349..354
FT	FT	Modified-site	/note= "predicted N-myristoylation site"
FT	FT	Modified-site	364..367
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	422..424
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	470..473
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	482..484
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	483..486
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	484..491
FT	FT	Modified-site	/note= "predicted tyrosine kinase phosphorylation site"
FT	FT	Modified-site	495..498
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
XX	XX		
XX	XX	WO200164905-A2.	
XX	XX	07-SEP-2001.	
XX	XX	28-FEB-2001; 2001WO-US006525.	

Query Match	99.4%	Score 2566	DB 4	Length 501
Best Local Similarity	99.6%	Pred. No. 6.5e-186		
Matches 499	Conservative 0	Mismatches 2	Indels 0	Gaps 0
1	MPEGCYLGRKKNVNOPESEVTDKYLQVTKTEFCEIPAKDKTGTGLTKCKFKRRDG			60
1	MFECVTLGDKKNVNOPESEVTDKYLQVTKTEFCEIPAKDKTGTGLTKCKFKRRDG			60
61	RKYAKAAKEIGILKMYKHPNLIQVDFVTRKKEFYFLELATGREVFDWILDGYSER			120
61	RKYAKAAKEIGILKMYKHPNLIQVDFVTRKKEFYFLELATGREVFDWILDGYSER			120
121	DTSNVVRQVLEAVYIHLTKIYHKNLKLNLVYNNRLKNSKIVISDFHLAKLENGLIKPE			180
121	DTSNVVRQVLEAVYIHLTKIYHKNLKLNLVYNNRLKNSKIVISDFHLAKLENGLIKPE			180
161	CGTEBYLAPEVVGORGRPYDCAIGIVYKYLISGNPPFEYEEEDDYENHDKNLPKRI			240
161	CGTEBYLAPEVVGORGRPYDCAIGIVYKYLISGNPPFEYEEEDDYENHDKNLPKRI			240
241	LAGEYFSPDWDISPAKDLVTRLMEVEEDQRIITAEALSHEMISGNAASDKNIKGV			300
241	LAGEYFSPDWDISPAKDLVTRLMEVEEDQRIITAEALSHEMISGNAASDKNIKGV			300
301	CAQCEKPNFARAKMKKAVRTTLMKRLPAPEOSSTAAASASATDTATPGAGATAAAS			360
301	CAQCEKPNFARAKMKKAVRTTLMKRLPAPEOSSTAAASASATDTATPGAGATAAAS			360
361	GATGAPEDBARAKSDNVAPADSSATPATDGSATPATDGSATPATDGSATPATDGSATP			420
361	GATGAPEDBARAKSDNVAPADSSATPATDGSATPATDGSATPATDGSATPATDGSATP			420
421	VTDSATPATDGRATPATSESTVTTQSSAMATKAAATPEPANAOPTSTAPGATGAP			480
421	VTDSATPATDGRATPATSESTVTTQSSAMATKAAATPEPANAOPTSTAPGATGAP			480
481	PSKGEBAAGYAQESQREAS 501			
481	PSKGEBAAGYAQESQREAS 501			

AC AAW93379;
 XX 06-NOV-2001 (first entry)
 XX Human polypeptide, SEQ ID NO: 2957.
 XX Human, full length cDNA; cDNA synthesis; oligo-capping.
 OS Homo sapiens.
 XX EPI130094-A2.
 XX EPI130094-A2.
 XX 05-SEP-2001.
 XX 07-JUL-2000; 2000EP-00114089.
 XX 08-JUL-1999; 99JP-00194486.
 XX 11-JAN-2000; 2000JP-00118774.
 XX 02-MAY-2000; 2000JP-00183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 DR N-PSDB; AAK94299.
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX Claim 8; SEQ ID NO 2957; 1380bp + Sequence Listing; English.
 XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesized by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 501 AA;
 Query Match 99.3%; Score 2563; DB 4; Length 501;
 Best Local Similarity 99.6%; Pred. No. 1.1e-165;
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGVYKTEEFCEIFRAKDKTTGKLTCKKFKQKRDG 60
 DB 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGVYKTEEFCEIFRAKDKTTGKLTCKKFKQKRDG 60
 QY 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120
 DB 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120
 QY 121 DTSNVVRQVLAVALYHSLKIVHNLKLENYVYNNRLKNSKIVISDPHLAKLENGLLKEP 180
 DB 121 DTSNVVRQVLAVALYHSLKIVHNLKLENYVYNNRLKNSKIVISDPHLAKLENGLLKEP 180
 QY 181 CGTPEYLAPEVVGQRQYRQYPCWAIGYVITLLSGNPPFEYEEEDDYENHNDLFRXI 240
 DB 181 CGTPEYLAPEVVGQRQYRQYPCWAIGYVITLLSGNPPFEYEEEDDYENHNDLFRXI 240
 QY 241 LAGDVEFDSPYWDIDISQAKDLVTRLMVEVEDORITAEALSHEMIISGNAASDNKIDGV 300
 DB 241 LAGDVEFDSPYWDIDISQAKDLVTRLMVEVEDORITAEALSHEMIISGNAASDNKIDGV 300
 QY 301 CAQIEKNFAPAKMKKAVRVTTLMKRLAPESOSTAAASASATDTATPGAAGATAAAS 360

DB 301 CAQIEKNFAPAKMKKAVRVTTLMKRLAPESOSTAAASASATDTATPGAAGATAAAS 360
 QY 361 GATSAPEDGAPAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 DB 361 GATSAPEDGAPAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTRDSATPATDGRATPATTEESTVPTTOSAMLATCAATPEPMAQPDSTAPEGATGAP 480
 DB 421 ATDRSATPATDGRATPATTEESTVPTTOSAMLATCAATPEPMAQPDSTAPEGATGAP 480
 QY 481 PSSKGEAAGYAQESQREAS 501
 DB 481 PSSKGEAAGYAQESQREAS 501
 RESULT 6
 ABUS2798
 ID ABUS2798 standard; protein; 473 AA.
 XX
 AC ABUS2798;
 XX
 DT 14-APR-2003 (first entry)
 XX Human signal transduction-associated protein from DXF2phb2_82e4.
 DE Human
 XX Human; gene therapy; vaccine; disease treatment; detection.
 OS Homo sapiens.
 XX
 PN WO200112659-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000MO-IB001496.
 XX
 PR 18-AUG-1999; 99US-0149499P.
 PR 28-SEP-1999; 99US-0156503P.
 XX
 PA (GEMU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S;
 XX
 DR WPI; 2001-327840/34.
 DR N-PSDB; ABX71280.
 XX
 PT Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies.
 XX
 PS Claim 21; Page 353; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a
 CC polypeptide described in the disclosure of the invention
 CC
 XX
 SQ Sequence 473 AA;
 Query Match 93.1%; Score 2403; DB 4; Length 473;
 Best Local Similarity 94.2%; Pred. No. 1.4e-173;
 Matches 472; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
 QY 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGVYKTEEFCEIFRAKDKTTGKLTCKKFKQKRDG 60
 DB 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGVYKTEEFCEIFRAKDKTTGKLTCKKFKQKRDG 60
 QY 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120

Db 61 RKVRKAANEIGILKVKHPNIIQLVDVFTREKREYFLELATGREVFDWILDQGYSER 120
 QY 121 DTSNVVRQVLEAVAYLHSLKIYHRNKLLENLYYNNRLKNSKIYISDPHLAKLENGLIKPEP 180
 Db 121 DTSNVVRQVLEAVAYLHSLKIYHRNKLLENLYYNNRLKNSKIYISDPHLAKLENGLIKPEP 180
 QY 181 CGPEYLAPEVVRGRGRPYDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
 Db 181 CGPEYLAPEVVRGRGRPYDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 212
 QY 241 LAGDYEFDSFYWMDISQAADLVTRIMEVEODQRTAEBAISHEMIISGNAASDKNIDGV 300
 Db 213 LAGDYEFDSFYWMDISQAADLVTRIMEVEODQRTAEBAISHEMIISGNAASDKNIDGV 272
 QY 301 CAQIEKNFAPAKKKAARVVTTLMKRLAPBOSSTAAQASATDTATPGAAGATATAAS 360
 Db 273 CAQIEKNFAPAKKKAARVVTTLMKRLAPBOSSTAAQASATDTATPGAAGATATAAS 332
 QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 Db 333 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 392
 QY 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAAATPEPMAQPDSTAPBEGATQAP 480
 Db 393 ATDRSATPATDGRATPATBESVPTTQSSAMLATKAAATPEPMAQPDSTAPBEGATQAP 452
 QY 481 PSSKGEAAGYAQESOREEAS 501
 Db 453 PSSKGEAAGYAQESOREEAS 473
 RESULT 7
 ID AAM93404 standard; protein; 470 AA.
 AC AAM93404;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide, SEQ ID NO: 3008.
 XX
 KM Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94325.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX
 PS Claim 8; SEQ ID NO 3008; 1380bp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5' and 3' ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful

CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 470 AA;
 Query Match 93.1%; Score 2402.5; DB 4; Length 470;
 Best Local Similarity 93.6%; Pred. No. 1.5e-173;
 Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;
 1 MPFGCVTLGDKKNTNQSSEYTDRLDQVITKEBFCEIFPAKKTCKLTKCKFKQRDQ 60
 1 MPFGCVTLGDKKNTNQSSEYTDRLDQVITKEBFCEIFPAKKTCKLTKCKFKQRDQ 60
 61 RKVRKAANEIGILKVKHPNIIQLVDVFTREKREYFLELATGREVFDWILDQGYSER 120
 61 RKVRKAANEIGILKVKHPNIIQLVDVFTREKREYFLELATGREVFDWILDQGYSER 120
 121 DTSNVVRQVLEAVAYLHSLKIYHRNKLLENLYYNNRLKNSKIYISDPHLAKLENGLIKPEP 180
 121 DTSNVVRQVLEAVAYLHSLKIYHRNKLLENLYYNNRLKNSKIYISDPHLAKLENGLIKPEP 180
 121 DTSNVVRQVLEAVAYLHSLKIYHRNKLLENLYYNNRLKNSKIYISDPHLAKLENGLIKPEP 180
 181 CGPEYLAPEVVRGRGRPYDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
 181 CGPEYLAPEVVRGRGRPYDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
 181 CGPEYLAPEVVRGRGRPYDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
 241 LAGDYEFDSFYWMDISQAADLVTRIMEVEODQRTAEBAISHEMIISGNAASDKNIDGV 300
 241 LAGDYEFDSFYWMDISQAADLVTRIMEVEODQRTAEBAISHEMIISGNAASDKNIDGV 300
 241 LAGDYEFDSFYWMDISQAADLVTRIMEVEODQRTAEBAISHEMIISGNAASDKNIDGV 300
 301 CAQIEKNFAPAKKKAARVVTTLMKRLAPBOSSTAAQASATDTATPGAAGATATAAS 360
 301 CAQIEKNFAPAKKKAARVVTTLMKRLAPBOSSTAAQASATDTATPGAAGATATAAS 360
 301 CAQIEKNFAPAKKKAARVVTTLMKRLAPBOSSTAAQASATDTATPGAAGATATAAS 360
 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 351 -----ADRSATPATDGSATPATDGSITPATDGSVTP 389
 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAAATPEPMAQPDSTAPBEGATQAP 480
 390 ATDRSATPATDGRATPATBESVPTTQSSAMLATKAAATPEPMAQPDSTAPBEGATQAP 449
 481 PSSKGEAAGYAQESOREEAS 501
 450 PSSKGEAAGYAQESOREEAS 470
 RESULT 8
 ID AAB20327 standard; protein; 470 AA.
 AC AAB20327;
 XX
 DT 29-MAY-2001 (first entry)
 DE Human protein phosphatase and kinase protein-6.
 XX
 KM Human protein phosphatase and kinase protein; PPHK-6; human;
 KM gastrointestinal disorder; immune system disorder; neurological disorder;
 KM cell proliferative disorder; cancer; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "O-phosphorylated"
 FT Modified-site 21 /note= "O-phosphorylated"
 FT Modified-site 21 /note= "O-phosphorylated"

FT Region 24. .286
 FT /note= "protein kinase signature"
 FT Domain 25. .276
 FT /note= "protein kinase domain signature"
 FT Modified-site 46
 FT /note= "O-phosphorylated"
 FT Modified-site 51
 FT /note= "O-phosphorylated"
 FT Modified-site 91
 FT /note= "O-phosphorylated"
 FT Modified-site 103
 FT /note= "O-phosphorylated"
 FT Modified-site 103
 FT /note= "O-phosphorylated"
 FT Modified-site 103
 FT /note= "O-phosphorylated"
 FT Modified-site 118
 FT /note= "O-phosphorylated"
 FT Domain 135. .153
 FT /note= "tyrosine kinase catalytic domain signature"
 FT Modified-site 135
 FT /note= "O-phosphorylated"
 FT Modified-site 138
 FT /note= "O-phosphorylated"
 FT Domain 201. .223
 FT /note= "tyrosine kinase catalytic domain signature"
 FT Modified-site 276
 FT /note= "O-phosphorylated"
 FT Modified-site 292
 FT /note= "O-phosphorylated"
 FT Modified-site 341
 FT /note= "O-phosphorylated"
 FT Modified-site 391
 FT /note= "O-phosphorylated"
 FT Modified-site 439
 FT /note= "O-phosphorylated"
 FT Modified-site 451
 FT /note= "O-phosphorylated"
 FT Modified-site 452
 FT /note= "O-phosphorylated"
 FT Modified-site 460
 FT /note= "O-phosphorylated"
 FT Modified-site 464
 FT /note= "O-phosphorylated"
 FT Modified-site /note= "O-phosphorylated"
 XX WO200120004-A2.
 XX 22-MAR-2001.
 XX 14-SEP-2000; 2000WO-US025515.
 XX 15-SEP-1999; 99US-0154141P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Yue H, Tang YT, Bandman O, Hillman JL, Baughn KR, Azimzai Y,
 PI Lu DM;
 DR WPI; 2001-244811/25.
 DR N-PSDB; AAF20381.
 XX
 PT Novel human protein phosphatase and kinase proteins for diagnosis,
 PT treatment and prevention of gastrointestinal, immune system, neurological
 PT and cell proliferative disorders.
 XX
 PS Claim 5; Page 89-90; 103pp; English.
 CC The present sequence is that of novel human protein phosphatase and
 CC kinase protein PPHKP-6, as predicted from Incyte Clone ID No. 1385073CB1
 CC (see AAF30481). Tissues that express PPHKP-6 (as a fraction of total
 CC tissues expressing PPHKP-6) include nervous (0.885) and developmental
 CC (0.077). Diseases or conditions associated with tissues expressing PPHKP-
 CC 6 (as a fraction of total tissues expressing PPHKP-6) include
 CC inflammation or trauma (0.384), neurological (0.231) and cancer (0.192).
 CC The encoded protein shows homology to rat calmodulin-binding protein. The

CC invention provides human PPHKP-1 to -11 polypeptides (see AAB20322-32)
 CC and polynucleotides (see AAF30476-86). It also provides expression
 CC vectors, host cells, antibodies, agonists and antagonists, as well as
 CC methods for diagnosing, treating or preventing disorders associated with
 CC expression of PPHKP, including gastrointestinal disorders, immune system
 CC disorders, neurological disorders and cell proliferative disorders.
 CC including cancer
 XX
 SQ Sequence 470 AA;
 Query Match 93.1%; Score 2402.5; DB 4; Length 470;
 Best Local Similarity 93.6%; Pred. No. 1.5e-173;
 Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;
 QY 1 MPFGCVTLGDKKNYNQSEVTRDYLQGVTKTEFCEIFRAKDTTGKLTCKKFKORDG 60
 DB 1 MPFGCVTLGDKKNYNQSEVTRDYLQGVTKTEFCEIFRAKDTTGKLTCKKFKORDG 60
 QY 61 RKVRKAANEIGILKMYGHPNLTQVDFVTRKKEVFIELATGREVDFWILDOGYYSER 120
 DB 61 RKVRKAANEIGILKMYGHPNLTQVDFVTRKKEVFIELATGREVDFWILDOGYYSER 120
 QY 121 DTSNVVRQVLEAVAYLHSLKIVHRNLTLENLVYNNRLKNSKIIVISDFHLAKLENGLIKEP 180
 DB 121 DTSNVVRQVLEAVAYLHSLKIVHRNLTLENLVYNNRLKNSKIIVISDFHLAKLENGLIKEP 180
 QY 181 CGTPEYLAPEVVGQRGRYPVDCALIGYINKTILSGNPPFEVEEDDYENHDKLFRKI 240
 DB 181 CGTPEYLAPEVVGQRGRYPVDCALIGYINKTILSGNPPFEVEEDDYENHDKLFRKI 240
 QY 241 LAGDYEPSPYWDIISQAKDLVRLMEVEDODQITAEALSHWISGNASDNKIDGV 300
 DB 241 LAGDYEPSPYWDIISQAKDLVRLMEVEDODQITAEALSHWISGNASDNKIDGV 300
 QY 301 CAQIEKNFARAKMKKAVVTTIMRLRAPBOSSYAAQASATDTATPGAAGCATPAAAS 360
 DB 301 CAQIEKNFARAKMKKAVVTTIMRLRAPBOSSYAAQASATDTATPGAAGCATPAAAS 360
 QY 361 GATSAPEGDAARAASDVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATP 420
 DB 361 GATSAPEGDAARAASDVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATP 420
 QY 421 VTRSATPATDGRATPATDESVPTTQSSAMLATKAAATPEPPMAAQDSTPEGATGAP 480
 DB 421 VTRSATPATDGRATPATDESVPTTQSSAMLATKAAATPEPPMAAQDSTPEGATGAP 480
 QY 481 PSSKGEAAGYAQESQREAS 501
 DB 481 PSSKGEAAGYAQESQREAS 501
 QY 450 PSSKGEAAGYAQESQREAS 470
 DB 450 PSSKGEAAGYAQESQREAS 470
 RESULT 9
 AAM93679
 ID AAM93679 standard; protein, 470 AA.
 XX
 AC AAM93679;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 3572.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 XX Homo sapiens.
 XX
 PN EP130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 XX
 PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isegai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR N-PSDB; AAK94614.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
in genetic manipulation.
PS Claim 8; SEQ ID NO 3572; 1380bp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
XX Sequence 470 AA;

Query Match 92.9%; Score 2398.5; DB 4; Length 470;
Best Local Similarity 93.4%; Pred. No. 3e-173;
Matches 468; Conservative 1; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKXNNOPSEVTDRLDGOVITKEEFCEIPRAKDKTTGKLTCKKFKORDG 60
DB 1 MPFGCVTLGDKKXNNOPSEVTDRLDGOVITKEEFCEIPRAKDKTTGKLTCKKFKORDG 60
QY 61 RRVKKAKEIGILKXVKNPILQVDFVTRKEVIFLELATGSEVDFMDLQGYSER 120
DB 61 RRVKKAKEIGILKXVKNPILQVDFVTRKEVIFLELATGSEVDFMDLQGYSER 120
QY 121 DTSNVRQVLEAVYVHSLKIYHRNKLENLYYRNKSKYIVISDFHLAKLENGIKEP 180
DB 121 DTSNVRQVLEAVYVHSLKIYHRNKLENLYYRNKSKYIVISDFHLAKLENGIKEP 180
QY 181 CGPEYLAPEVVGROGRPVOCWALGVIMYILSGNPFYEEVEDDVENHDKLPRKI 240
DB 181 CGPEYLAPEVVGROGRPVOCWALGVIMYILSGNPFYEEVEDDVENHDKLPRKI 240
QY 241 IAGDYFDSFYWDISQAADLVTRIMEYBODRITAEBAISHWISGNAASDKXIKDGV 300
DB 241 IAGDYFDSFYWDISQAADLVTRIMEYBODRITAEBAISHWISGNAASDKXIKDGV 300
QY 301 CAQIEKNFAPAKKKAVRVTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
DB 301 CAQIEKNFAPAKKKAVRVTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
QY 361 GATSAPEGDAARAASNDNAPADRSATPATDGSATATGSGVTPADGSIPTATGSVTP 420
DB 361 GATSAPEGDAARAASNDNAPADRSATPATDGSATATGSGVTPADGSIPTATGSVTP 420
QY 421 VTDRSATPATDGSATATGSGVTPATGSGVTPATGSGVTPATGSGVTPATGSGVTP 480
DB 421 VTDRSATPATDGSATATGSGVTPATGSGVTPATGSGVTPATGSGVTPATGSGVTP 480
QY 481 PSSKGEBAAGYAOESQREAS 501
DB 481 PSSKGEBAAGYAOESQREAS 501
QY 490 PSSKGEBAAGYAOESQREAS 470
DB 490 PSSKGEBAAGYAOESQREAS 470

RESULT 10
AAM38987

ID AAM38987 standard; protein; 470 AA.
XX
XX AAM38987;
AC
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 2132.
DE
XX

Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200153312-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000MO-US034263.
PF
XX
XX 23-DEC-1999; 99US-00471275.
PR
XX 21-JAN-2000; 2000US-00488725.
PR
XX 25-APR-2000; 2000US-00552317.
PR
XX 20-JUN-2000; 2000US-00598042.
PR
XX 19-JUL-2000; 2000US-00620312.
PR
XX 03-AUG-2000; 2000US-00653450.
PR
XX 14-SEP-2000; 2000US-00662191.
PR
XX 19-OCT-2000; 2000US-00693036.
PR
XX 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;
PI Zhou P, Goodrich R, Dmanac RT;
XX
XX WPI; 2001-442253/47.
DR
XX N-PSDB; AAI58143.
DR
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.
PT
XX
XX Example 4; SEQ ID NO 2132; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AA42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 470 AA;

Query Match 92.7%; Score 2391.5; DB 4; Length 470;
Best Local Similarity 93.2%; Pred. No. 1e-172;
Matches 467; Conservative 1; Mismatches 2; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKXNNOPSEVTDRLDGOVITKEEFCEIPRAKDKTTGKLTCKKFKORDG 60
DB 1 MPFGCVTLGDKKXNNOPSEVTDRLDGOVITKEEFCEIPRAKDKTTGKLTCKKFKORDG 60

KM endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
 KM respiratory disorder; renal disorder; kidney failure; blood disorder;
 KM myocardial infarction; wound healing; cell proliferation; skin aging;
 KM food additive; food preservative; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155318-A2.
 PD
 XX 02-AUG-2001.
 PF 17-JAN-2001; 2001WO-US001332.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218250P.
 PR 26-JUL-2000; 2000US-0220563P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
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 PR 14-AUG-2000; 2000US-0225270P.
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 PR 18-AUG-2000; 2000US-0226279P.
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 PR 23-AUG-2000; 2000US-0227009P.
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 PR 01-SEP-2000; 2000US-0229287P.
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 PR 01-SEP-2000; 2000US-0229344P.
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 PR 05-SEP-2000; 2000US-0229509P.
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 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
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 PR 08-SEP-2000; 2000US-0232081P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
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 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-024475P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
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 PR 17-NOV-2000; 2000US-0249210P.
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 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251859P.
 PR 08-DEC-2000; 2000US-0251999P.

PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0234984P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
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 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
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 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251889P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-465460/50.
 DR N-PSDB; AAS27184.
 XX
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders.
 XX
 PS Claim 1, SEQ ID NO 832; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
 CC (Down syndrome), ischemic injury (e.g. stroke), renal disorders (e.g.
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
 CC respiratory disorders, dermatological disorders, in wound healing,
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
 CC disease), reproductive system disorders, gastrointestinal disorder
 CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce
 CC higher affinity antibodies, and as a means to induce tumour proliferation
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
 CC AAU17683 represent novel signal transduction pathway protein, amino acid
 CC sequences of the invention
 XX

Query Match 33.0%; Score 852; DB 4; Length 219;
 Best Local Similarity 72.6%; Pred No. 1.9e-56;
 Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;
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 Db :::
 14 FVAPEVVGQRGRYPVCAIVIMYLLSGNPPEVEEEDDYENHDKNLEFKILLAGDY 73
 QY 246 EPDSEPYWDDISQAADLVTRLMVEVRODRTAEKAIISHMISGNAASDKNTKGVCAQIE 305
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 Db :::
 134 KNFAPAKWKKAIVRTTLMRLAPROSSAAQOSASDTATPAGAGATATAAAGANSA 178
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 Db :::
 179 -----ADKCPQPGQMEVFPQPLAAVSPQPMEMASXKPLMGSVTPA 219

Search completed: April 23, 2004, 15:48:15
 Job time : 62 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 23:13:47 ; Search time 7605 Seconds

(without alignments)
12266.858 Million cell updates/sec

Title: US-10-669-689-1

Perfect score: 3124
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Sequence: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_estbm:*
3: em_estbn:*
4: em_estbu:*
5: em_estbv:*
6: em_estbl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfm:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vil:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1691.8	54.2	3692 11	AK085143 Mus muscu
2	1060	33.9	1201 13	BX418741 BX418741
3	1013.2	32.4	1201 13	EX374857 EX374857
4	1000	32.0	1201 9	AL539856 AL539856

5	978	31.3	1201 13	BX418742	AK085143	3692 bp	mRNA	linear	HTC 20-SEP-2003
6	976	31.2	1201 13	AL568077	AK085143				
7	951	30.4	1201 13	BX440618					
8	937.6	30.0	1027 18	BX460352					
9	932.4	29.8	1201 9	AL568260					
10	911.4	29.2	1201 13	BX461112					
11	906.8	29.0	1201 13	BX460131					
12	901.8	28.9	964 13	BX425447					
13	896.8	28.7	911 13	BX353478					
14	875.4	28.0	955 13	BX353479					
15	867.6	27.8	1201 13	BX423239					
16	856.8	27.4	1158 9	AL527582					
17	844	27.0	930 13	BX460569					
18	843	27.0	1201 9	AL540163					
19	829	26.5	955 13	BX419372					
20	815	26.1	1014 13	BX460351					
21	808.8	25.9	963 13	BX425446					
22	777	24.9	778 13	BX094603					
23	776.6	24.9	923 13	BX176428					
24	774.8	24.8	894 9	AL534083					
25	766.2	24.5	872 12	B1544594					
26	761.2	24.4	1201 13	BX460130					
27	747.6	23.9	841 12	B1917571					
28	740.8	23.7	996 12	B1755292					
29	735.2	23.5	904 9	AL534084					
30	733.8	23.5	802 12	B1600132					
31	725.4	23.2	1166 9	AL527583					
32	721.4	23.1	849 12	B1597484					
33	720.2	23.1	917 13	BX419371					
34	712.2	22.8	784 10	BX798859					
35	712	22.8	794 12	B1758188					
36	710.2	22.7	1201 13	BX423240					
37	709.2	22.7	835 12	B1757754					
38	685	21.9	718 12	BX700838					
39	681	21.8	720 12	BX704846					
40	679.8	21.8	723 10	BX790638					
41	670	21.4	725 12	BX700874					
42	666.2	21.3	963 10	BX797447					
43	661	21.2	673 14	BX155378					
44	654.4	20.9	656 12	BX665442					
45	654.4	20.9	764 12	B1603102					

ALIGNMENTS

RESULT 1
AK085143
LOCUS
DEFINITION
AK085143
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone: D330043A01 product: SIMILAR TO VESICLE-ASSOCIATED CALMODULIN-BINDING PROTEIN homolog [Mus musculus], full insert sequence.
ACCESSION
AK085143
VERSION
AK085143.1 GI:26102493
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PubMed
10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374

REFERENCE	PUBMED	11042159
REFERENCE	AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishik, K., Kitsumaru, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujimake, S., Inoue, K., Togawa, Y., Iwasa, M., Ohara, E., Washikita, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	6 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	6 (bases 1 to 3692) Adachi, J., Aizawa, K., Akimura, T., Aakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizumoto, K., Hiroaka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishik, K., Nomura, K., Numasaki, R., Ohno, M., Ohse, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sobue, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	Direct Submission Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of Physiological and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	1. 3692 /organism="Mus musculus" /mol_type="mRNA" /strain="CS7BL/6J" /db_xref="PANTOM:DB:0430043A01" /db_xref="MGI:2422056" /db_xref="taxon:10090" /clone="D430043A01" /tissue_type="lung" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="13 days embryo"
JOURNAL	MEDLINE	20530913
REFERENCE	PUBMED	11076861
REFERENCE	AUTHORS	misc_feature 1. 3692 /note="SIMILAR TO VESTICLE-ASSOCIATED CALMODULIN-BINDING PROTEIN homolog [Mus musculus] (SPR1AAH17634, evidence: FASTA, 93.8%ID, 100%length, match=1539)"
JOURNAL	MEDLINE	20530913
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REFERENCE	AUTHORS	Query Match 54.2%; Score 1691.8; DB 11; Length 3692;

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Matches 2422; Conservative 0; Mismatches 514; Indels 173; Gaps 25;	
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Db	113 CTGCTGTGACCGACCAAGCTTTC-----AGAGCTAGCAATGCCGTTTGGTGTGAC 167
QY	231 TCTGGCGGACAGAGAACTATTAACAAGCATGAGGTGACTGACAGATATGATTTGGG 290
Db	168 TCTGGGTGACAAAGAAAGAACTATTAACAGCCATCGGAAGTACTGACAGATATGACTGGG 227
QY	291 ACGAGTCAATAACACTGAGAGATTTTGTGAATCTTCCGGGCCAAGACAAAGACGACAG 350
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QY	351 CAAGCTGCACACCTGCAGAAAGTTCCAGAAAGCGGACGCGCAAGGTGTGGAAAGCTGC 410
Db	288 CAAGCTGCACACCTGTAGAAAGTTCCAGAAAGCTGATGGCGCAAGGTGTGGAAAGCAGC 347
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Db	348 CAAGAACGAGATAGGAAATCTCAAGATGTGAAAGCACTCCCAACATCCTGACGCTGTAGA 407
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Db	408 TGTGTTTGTGACCCGCAAGAGATACTTCACTTCTGTGAGCTGGCCACCGGAGAGGAGGT 467
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 QY 503 TCTCGAGCTGGCCACGGGGAGGGAGGTGTTGACTGGATCTCGACAGGGCTACTTACT 562
 DB 488 TCTCGAGCT-----GGCTACTACT 507
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 ACCESSION AL568077
 VERSION AL568077.2 GI:31290926
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12922074.
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1934.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF031CD08NP1&cluster=1934.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF031CD08NP1.
 FEATURES
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 location/Qualifiers
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 /clone="CS0DF031YH15"
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 /clone_1ib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
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 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 ORIGIN
 Query Match 31.2%; Score 976; DB 9; Length 1201;
 Best Local Similarity 98.9%; Pred. No. 5e-123;
 Matches 981; Conservative 9; Mismatches 1; Indels 1; Gaps 1;
 QY 2022 GGGGCTCCGCTGCTCCTTCCCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2081
 DB 991 GGGGCTCCGCTGCTCCTTCCCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
 QY 2082 CAGGTCCCACTCTCCCAAGGCGCTTAACTTGGGCGGCTTGGCTGAGCTGCTGCTGCTGCTG 2141
 DB 931 CAGGTCCCACTCTCCCAAGGCGCTTAACTTGGGCGGCTTGGCTGAGCTGCTGCTGCTGCTG 872
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 DB 871 CAGCGAGGCGCTGTGAGGCGCTTAACTTGGGCGGCTTGGCTGAGCTGCTGCTGCTGCTGCTG 812
 QY 2202 TGGGCTGCTGTGAGGCGCTTAACTTGGGCGGCTTGGCTGAGCTGCTGCTGCTGCTGCTG 2261
 DB 811 TGGGCTGCTGTGAGGCGCTTAACTTGGGCGGCTTGGCTGAGCTGCTGCTGCTGCTGCTGCTG 752
 QY 2262 GTTTAAGTCCAGACTTGGGCACTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2321
 DB 751 GTTTAAGTCCAGACTTGGGCACTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
 QY 2322 GAGTGAGAGAGATGATGAGAGGCGAAGGCTTCATTTTGTCTTCTTAAGACCTTG 2381
 DB 691 GAGTGAGAGAGATGATGAGAGGCGAAGGCTTCATTTTGTCTTCTTAAGACCTTG 632
 QY 2382 TTATTTGTGTTATTTCTGCTTCTTCCGAGTCTGCAAGTGGGCTGCTGCTGCTGCTGCTG 2441
 DB 631 TTATTTGTGTTATTTCTGCTTCTTCCGAGTCTGCAAGTGGGCTGCTGCTGCTGCTGCTG 572
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 DB 511 AGAGTCAAGCCAGACCAAGTGTCCAGCTTACTGAGTCTTAACTTCCCTGAGGCAAAACA 452
 QY 2562 GGGAGGCTGATACCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2621
 DB 451 GGGAGGCTGATACCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 392

QY 2622 AGTCTCTCCACCCCTAGGGGGCTTGTGCATGGCAATACATCATATGATTTGAGGT 2681
 DB 391 AGTCTCTCCACCCCTAGGGGGCTTGTGCATGGCAATACATCATATGATTTGAGGT 332
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 DB 331 TTGACCTTACAGGGGAGATTTTCTGCTCACTTCAACATGAATGAAGAGAACTCCC 272
 QY 2742 TCTTTCTACAGCTCACTTCTATCAGAGGCCAGGCTCTCAGAGCCATTTAGTTGCTT 2801
 DB 271 TCTTTCTACAGCTCACTTCTATCAGAGGCCAGGCTCTCAGAGCCATTTAGTTGCTT 212
 QY 2802 TTTCTGGAGTGAAGAAAGTAACTTAACTCCCACTTTCTGAGGAGAGCTCTGACAGG 2861
 DB 211 TTTCTGGAGTGAAGAAAGTAACTTAACTCCCACTTTCTGAGGAGAGCTCTGACAGG 152
 QY 2862 TGCCCTTTGTGACAGCCCTACACAGCTGGATAGGAGAGCAATTTGCTCGCCCTTGC 2921
 DB 151 TGCCCTTTGTGACAGCCCTACACAGCTGGATAGGAGAGCAATTTGCTCGCCCTTGC 92
 QY 2922 TCGGCACTCTGAGTGTCTGCTCCCTTCTCTCTGATGCTGTGGGTCTGCTGTGTG 2981
 DB 91 TCGGC-CTCCGTGTGTGTGTCTCCCTTCTCTCTGATGCTGTGGGTCTGCTGTGTG 33
 QY 2982 TGAAGTCGAGTGGTTAACTGTGTGCTTACTG 3013
 DB 32 TGAAGTCGAGTGGTTAACTGTGTGCTTACTG 1
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 LOCUS BX440618 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF009Y013 3-PRIME, mRNA sequence.
 ACCESSION BX440618
 VERSION BX440618.1 GI:30771860
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 invitrogen. This sequence belongs to sequence cluster 1934.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF009AH07NP1&cluster=1934.r. Contact :
 Feng Liang Email: fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paradise Avenue Genoscope sequence ID : CS0DF009AH07NP1.
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 /mol_type="mRNA"
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 /rname="FETAL BRAIN"
 /dev_stage="fetal"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo (dT) primer, 5' end
 enriched, double-strand cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 FEATURES
 source

Query Match 30.4%; Score 951; DB 13; Length 1201;
 Best Local Similarity 92.0%; Pred. No. 1.2e-119;
 Matches 994; Conservative 17; Mismatches 69; Indels 1; Gaps 1;
 QY 1929 CGAGCCCTGACAGATTCCTTGTGCTTTCTGTCTTTGCTAGCTTACCAAGTTTCG 1988
 DB 1101 CGAGCCCTGACAGATTCCTTGTGCTTTCTGTCTTTGCTAGCTTACCAAGTTTCG 1042
 QY 1989 TTTCTGTGAGATGCTCTTGTAGGATCTCAAGGGGGCTCTGCTCTCCCTTCCC 2048
 DB 1041 TTTCTGTGAGATGCTCTTGTAGGATCTCAAGGGGGCTCTGCTCTCCCTTCCC 982
 QY 2049 TTTCTGTGAGATGCTCTTGTAGGATCTCAAGGGGGCTCTGCTCTCCCTTCCC 2108
 DB 981 TTTCTGTGAGATGCTCTTGTAGGATCTCAAGGGGGCTCTGCTCTCCCTTCCC 922
 QY 2109 ACTTGGGCGGCTTGTGCTGAGAGCTGTCTCAGAGGCTCTTCAAGGCTCTTAAG 2168
 DB 921 ACTTGGGCGGCTTGTGCTGAGAGCTGTCTCAGAGGCTCTTCAAGGCTCTTAAG 862
 QY 2169 CTCTGTGACATGAAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2228
 DB 861 CTCTGTGACATGAAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 802
 QY 2229 TGTGTATGAGATGCAAGAAAGTAAAGGCAATATTTAAAGTCCAGACTTGGCAGATGGCT 2288
 DB 801 TGTGTATGAGATGCAAGAAAGTAAAGGCAATATTTAAAGTCCAGACTTGGCAGATGGCT 742
 QY 2289 AGGATATCTGCTCACTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
 DB 741 AGGATATCTGCTCACTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 682
 QY 2349 GAACTTCCATTTTGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2408
 DB 681 AAGCTTCCATTTTGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 622
 QY 2409 AGTCTGTGAGT 2468
 DB 621 AGTCTGTGAGT 562
 QY 2469 CAATTAGAGCTGTGCAATGAGACCTGTGAGAGGAGTACAGCCAGCAAGGATGTCC 2528
 DB 561 CAATTAGAGCTGTGCAATGAGACCTGTGAGAGGAGTACAGCCAGCAAGGATGTCC 502
 QY 2529 CAGCTTACTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2588
 DB 501 CAGCTTACTGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 442
 QY 2589 CTAGATGCCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2648
 DB 441 CTAGATGCCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 382
 QY 2649 GCAATGCGAATATCATATATGATTTGAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTG 2708
 DB 381 GCAATGCGAATATCATATATGATTTGAGAGTGTGCTTCTTCTTCTTCTTCTTCTTCTG 322
 QY 2709 CTGAGTTCAACATGAATGAAGAACTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTGAG 2768
 DB 321 CTGAGTTCAACATGAATGAAGAACTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTGAG 262
 QY 2769 GCCAGGTGCTCAGAGCCACATTAAGTTGCTTTTCTGAGATGAAGAAAGTAAAGTTTAA 2828
 DB 261 GCCAGGTGCTCAGAGCCACATTAAGTTGCTTTTCTGAGATGAAGAAAGTAAAGTTTAA 202
 QY 2829 CTCCTCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2888
 DB 201 CTCCTCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 142
 QY 2889 TGGATAGGAGCAGATTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2948
 DB 141 TGGATAGGAGCAGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 83

[illegible]

RESULT	8
LOCUS	BX460352
DEFINITION	BX460352 Homo sapiens FETAL BRAIN Hom sapiens cDNA clone
FEATURES	CSDPFL13YC02 5-PRIME, mRNA Sequence.
ORIGIN	1027 bp mRNA linear EST 22-MAY-2003

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Ukaiyotai; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1027) Jeessee, J. and Polayevs, D. Full-length cDNA libraries and normalization unpublished (2001)
REVIEW	
COMMENT	Contact: Genoscope W44000@dsi.jussieu.fr

BP 191 91006 Evry cedex - France
Email: segrete@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1934.r For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF013BB01Q1&cluster=1934.r>. Contact :
Peng Liang Email : liangpeng@lifetech.com URL :
<http://fulllength.invitrogen.com/invitrogen/Corporation/1600>
Faraday Avenue Genoscope sequence ID : CS0DF013BB01Q1.
location:Oval1ffiers

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/organism="Homo sapiens"
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/clone="CSDDP013YC02"
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/dev_stage="fetal"
/clone_id="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

```

	Query Match	30.0%; Score 937.6; DB 13; Length 1027;
	Best Local Similarity	98.0%; Pred. No. 8.5e-118;
	Matches	953; Conservative 13; Mismatches 4; Indels 2; Gaps 2;
QY	52 CTGAGGTTGGCTTACCGGAGCGGCTGCATCTGGCGCGGCTCTGGCCCCGGTGTCTGGGA	111
Db	57 CGGATGTTCCCTATGCGCCAGACGCGCTGCATCTGGCGCGCGCTGTGCS	116
QY	112 GGGATTCTGGCCCGCGCGTCCCCGGAGGCGCTGGGGCGCGCGGTGAGCCGGCGATCACTTCC	171
Db	117 GCGATTCTGCCCGCGCGTCTCCCGGAGCCCTGGCGCGCCCGCTGAGCCCGCGATCACTTCC	176
QY	172 TCCCTGTGACCAACCGGCGCTGCGAGGTGAGAGCTTGAGATGCCCTTTTGAGTGTGACT	231
Db	177 TCCCTGTGACCAACCGGCGCTGCGAGGTGAGAGCTTGAGATGCCCTTTTGAGTGTGACT	236
QY	232 CTGGGCGGAGAGAGACTATTAACCGCCATCGAGGTGACTGAC-AGATATGATTTGGG	290
Db	237 CTGGGCGGAGAGAGANTATTAACCGCCATCGAGGTGACTGACGAGATATGATTTGGG	296

QY	291	CAAGGTATCAAAAGCTGAGAGAGTTTGTGTAATCTTCGGGGCCAAAGGACAGAGACGACAGG	350
Db	297	ACAGGTATCAAAAGCTGAGAGAGTTTGTGTAATCTTCGGGGCCAAAGGACAGAGACGACAGG	356
QY	351	CAAGCTCACACCTGCAAGAGTTTCAGAAAGCGGAGCGCCAGAGTCCGGAAGCTGC	410
Db	357	CAAGCTCACACCTGCAAGAGTTTCAGAAAGCGGAGCGCCAGAGTCCGGAAGCTGC	416
QY	411	CAGAACGAGATAGGCACTCTCAAGTGGTGAAGATCCCAATCCTACAGCTGTGGA	470
Db	417	CAGAACGAGATAGGCACTCTCAAGTGGTGAAGATCCCAATCCTACAGCTGTGGA	476
QY	471	TGTGTTGTGATCCCGCAAGGAGTACTTATCTTCTCTGAGCTGGCACGGGGAGAGGT	530
Db	477	TGTGTTGTGATCCCGCAAGGAGTACTTATCTTCTCTGAGCTGGCACGGGGAGAGGT	536
QY	531	GTTTGATCGATCTCTGATCCAGAGGCTCATCTCTCGGAGGGAGACACAAACCAAGTGGTACG	590
Db	537	GTTTGATCGATCTCTGATCCAGAGGCTCATCTCTCGGAGGGAGACACAAACCAAGTGGTACG	596
QY	591	GCAAGTCTGAGAGCGGTGGCCATTGTAAGTCACTCAAGATCGTGACAGAGAACTCTCAA	650
Db	597	GCAAGTCTGAGAGCGGTGG3-CYATTGTCATCTCAAGATCGTGACAGAGAACTCTCAA	655
QY	651	GCTGAGAAACCTGGTTTACTACAAACCGGCTGAAGAACTCGAAGATTGTCATCAGTGACTT	710
Db	656	GCTGAGAAACCTGGTTTACTACAAACCGGCTGAAGAACTCGAAGATTGTCATCAGTGACTT	715
QY	711	CCATCTGGCTAAGCTAGAAAATGGCTCATCAAGAGGCGCTGTGGACCCCGAGTATCT	770
Db	716	CCATCTGGCTAAGCTAGAAAATGGCTCATCAAGAGGCGCTGTGGACCCCGAGTATCT	775
QY	771	GGCCCCAGAGGTGGTAGGCGGCGGACGGGTATGAGCGCCCTGTGACTGTGGCCATTGG	830
Db	776	GGCCCCAGAGGTGGTAGGCGGCGGACGGGTATGAGCGCCCTGTGACTGTGGCCATTGG	835
QY	831	AGTATATATGTAATCTCTGCTTCAGGCAATCACTTTCTATGAGAGGTGGAAAGAA	890
Db	836	AGTATATATGTAATCTCTGCTTCAGGCAATCACTTTCTATGAGAGGTGGAAAGAA	895
QY	891	TGATTATGAAACCATGATAGAAATCTCTCGCAAGATCCGAGGTGTGACTATAGTT	950
Db	896	TGATTATGAAACCATGATAGAAATCTCTCGCAAGATCCGAGGTGTGACTATAGTT	955
QY	951	TGACTCTCCATATTGGGATGATATTTCGAGGACAGCAAGACTGTGCACAGAGCTGAT	1010
Db	956	TGACTCTCCATATTGGGATGATATTTCGAGGAGCAGCAAGACTGTGCATMAAGCTGAT	1015
QY	1011	GAAGGTGAGACA 1022	
Db	1016	GGGGGAGACACA 1027	

RESULT 9	1201 bp	mRNA	linear	EST 31-MAY-2003
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LOCUS				
DEFINITION	1201 bp	mRNA	linear	EST 31-MAY-2003
ACCESSION	AL568260	Homo sapiens FETAL BRAIN	Homo sapiens cDNA	clone
VERSION	CS0DFO3212011.3-PRIME	mRNA sequence.		
KEYWORDS	AL568260			
SOURCE	AL568260.2	GI:31291103		
ORGANISM	EST.			
	Homo sapiens (human)			
	Homo sapiens			
REFERENCE	RukayaYota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 1201)			
JOURNAL	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.			
COMMENT	Full-length cDNA libraries and normalization			
	Unpublished (2001)			
	On Feb 16, 2001 this sequence version replaced gi:12922422.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	BP 191 91006 Evry cedex - France			

Query Match 29.2%; Score 911.4; DB 13; Length 1201;
 Best Local Similarity 97.7%; Pred. No. 2,9e-114;
 Matches 931; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

QY 98 CCGCGCTGCTGGAGCGGATTTCTGCCCCGCTGCCGAGACCTCCGCGCCCGCTGAGC 157
 Db CCGCGGATCTTCGAGCGGATTTCTGCCCCGCTGCCGAGACCTCCGCGCCCGCTGAGC 119
 QY 158 CCGCGATCACTTCTCCCTGTGACCAACCGCGCTGAGGTTGAGGCTGAGCAATCGCT 217
 Db CCGCGATCACTTCTCCCTGTGACCAACCGCGCTGAGGTTGAGGCTGAGCAATCGCT 179
 QY 218 TTGGGTGTGTGACTCTGGGCGCAAGAAAGACTTAACAGCCATCGAGGTGATGACA 277
 Db TTGGGTGTGTGACTCTGGGCGCAAGAAAGACTTAACAGCCATCGAGGTGATGACA 239
 QY 278 GATATGATTTGGGACAGGTCTCAAGACTGAGAGTTTGTAAATCTTCGCGCCCAAG 337
 Db GATATGATTTGGGACAGGTCTCAAGACTGAGAGTTTGTAAATCTTCGCGCCCAAG 299
 QY 338 ACAAGAGACAGGCAAGCTGACACTCTGCAAGAAAGTTCCAGAAAGCGGAGCGCGCAGG 397
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 QY 458 TACAGCTGTGATGTGTTGTGACCCGCAAGAGATCTTATCTTCCTGAGCTGAGCA 517
 Db TACAGCTGTGATGTGTTGTGACCCGCAAGAGATCTTATCTTCCTGAGCTGAGCA 479
 QY 518 CGGAGAGGAGGTGTTGATCTGATCTGCAACAGGCTACTACTCGAGCGAGACACAA 577
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 QY 578 GCACATGTGTACGGCAAGTCTCTGAGGCGCTGAGCTATTGCACTCACTCAAGATCGTGC 637
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 QY 638 ACAGGAATCTCAAGCTGAGAGACCTGTTTACTCAACCGGCTGAGAGATCGAAGATTG 697
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 QY 698 TCATCAATGATCTTCATCTGCTAAGCTAAGAAATGAGCTCATCAAGAGAGCTCTGAGGA 757
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 QY 938 GTGACTATGATTTGATCTTCCATA-TTGGGATGATTTTGGCAGGAGCCAAAGACCTG 996
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RESULT 11
 LOCUS BX460131 1201 bp mRNA linear EST 22-MAY-2003
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 VERSION BX460131 GI:31023203
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li W.B., Gruber C., Jessee J., and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1934.r for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF011Y20&cluster=1934.r. Contact:
 Feng Liang Email: fliang@lifeotech.com URL: Corporation 1600
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
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 /note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 29.0%; Score 906.8; DB 13; Length 1201;
 Best Local Similarity 98.1%; Pred. No. 1.2e-113;
 Matches 942; Conservative 6; Mismatches 8; Indels 4; Gaps 3;

QY 63 CTAGCGGAAGCGGCTGATCTGAGCGCGCTGCTGCCGCTGAGAGCGGATTTCTG 122
 Db CTAGCGGAAGCGGCTGATCTGAGCGCGCTGCTGCCGCTGAGAGCGGATTTCTG 129
 QY 123 CCGCGCTCCCCGAGAGCCCTCGGCGCCCGCTGAGCCCGGATCACTTCCCTGTGAGC 182
 Db CCGCGCTCCCCGAGAGCCCTCGGCGCCCGCTGAGCCCGGATCACTTCCCTGTGAGC 189
 QY 130 CCGCGCTCCCCGAGAGCCCTCGGCGCCCGCTGAGCCCGGATCACTTCCCTGTGAGC 189
 Db CCGCGCTCCCCGAGAGCCCTCGGCGCCCGCTGAGCCCGGATCACTTCCCTGTGAGC 189
 QY 183 AACCGGCGTGAAGTGAAGCTGAGCAATGCGGTTTGGGTGTGATCTGAGCGACAA 242
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 QY 190 AACCGGCGTGAAGTGAAGCTGAGCAATGCGGTTTGGGTGTGATCTGAGCGACAA 249
 Db AACCGGCGTGAAGTGAAGCTGAGCAATGCGGTTTGGGTGTGATCTGAGCGACAA 249
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 Db GAAGAACTAATACCAAGCAATCGAGGTGACTGACAGATTAATTTGGGACAGTCA 309
 QY 250 GAAGAACTAATACCAAGCAATCGAGGTGACTGACAGATTAATTTGGGACAGTCA 309
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 QY 303 GACTGAGAGTTTGTGAAATCTTCCGGGCAAGAGCAAGAGCAAGAGTGTGAC 362
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 QY 310 GACTGAGAGTTTGTGAAATCTTCCGGGCAAGAGCAAGAGCAAGAGTGTGAC 369
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 QY 423 AGGCATCTCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGATGTGTTGTGAC 482
 Db AGGCATCTCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGATGTGTTGTGAC 489
 QY 430 AGGCATCTCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGATGTGTTGTGAC 489
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 QY 483 CCGCAAGAGTACTTATCTTCTGAGAGCTGCGCACGCGGAGGAGGTGTTTGTGATGAT 542
 Db CCGCAAGAGTACTTATCTTCTGAGAGCTGCGCACGCGGAGGAGGTGTTTGTGATGAT 542

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Db      |||||
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Qy      |||||
543 CCTGAGCCAGGAGCTACTACTCGAGAGGAGACACAAGCAACGTGTACCGCAAGTCTTGA 602
Db      |||||
550 CTTGAGCCAGGAGCTACTACTCGAGAGGAGACACAAGCAACGTGTACCGCAAGTCTTGA 609
Qy      |||||
603 GGCCGTGGCTTATTTGCACTCACTCAAGTCTGTGACAGAGAAATCTCAAGCTGGAGAACT 662
Db      |||||
610 GGCCGTGGCTTATTTGCACTCACTCAAGTCTGTGACAGAGAAATCTCAAGCTGGAGAACT 669
Qy      |||||
663 GGTTCATCTCAACCGGCTAAGAGATCTGAAGATTTGATCATAGTACTTCCATCTGGCTAA 722
Db      |||||
670 GGTTCATCTCAACCGGCTAAGAGATCTGAAGATTTGATCATAGTACTTCCATCTGGCTAA 729
Qy      |||||
723 GGTAGAAATGGGCTCATAGAGAGCCCTGTGGAGACCCCGAGTATCTGGCCCGAGAGGT 782
Db      |||||
730 GGTAGAAATGGGCTCATAGAGAGCCCTGTGGAGACCCCGAGTATCTGGCCCGAGAGGT 789
Qy      |||||
783 GGTAGGCGGAGAGGCTATGAGAGCCCTGTGGAGTCTGGCCATTGGAGTCAATCATGTA 842
Db      |||||
790 GGTAGGCGGAGAGGCTATGAGAGCCCTGTGGAGTCTGGCCATTGGAGTCAATCATGTA 849
Qy      |||||
843 CATCTGCTTTCAGGCAATCCACCTTTCTATGAGAGAGGTGAGAGAGATGATTATGAGAA 902
Db      |||||
850 CATCTGCTTTCAGGCAATCCACCTTTCTATGAGAGAGGTGAGAGAGATGATTATGAG-A 908
Qy      |||||
903 CATGATAGAGATCTTCTTCCGCAAGTCTGTGCTGTGATCTATGAGTTTGAATCTCCATA 962
Db      |||||
909 KCATGATAGAGATCTTCTTCCGCAAGTCTGTGCTGTGATCTATGAGTTTGAATCTCCATA 968
Qy      |||||
963 TTGGAGTATATTTTGGCAGAGCAGCAAGACCTGTGATCAAGAGCTGATGAGAGAGAGCA 1022
Db      |||||
969 TTGGAGTATATTTTGGCAGAGCAGCAAGACCTGTGATCAAGAGCTGATGAGAGAGAGCA 1025

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RESULT 12
BX425447      964 bp      mRNA      linear      EST 15-MAY-2003
LOCUS      BX425447 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION      BX425447
ACCESSION      BX425447
VERSION      BX425447
KEYWORDS      BX425447.1 GI:30782455
SOURCE      EST.
ORGANISM      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
            1 (bases 1 to 964)
            Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
            Full-length cDNA libraries and normalization
            unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1934.r for
            more information about this cluster, see
            http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CL08B014ZE06R1&cluster=1934.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CL08B014ZE06R1.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL08B014ZE06"
/cisue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

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with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

```

ORIGIN
Query Match      28.3%; Score 901.8; DB 13; Length 964;
Best Local Similarity 97.6%; Freq. No. 6, 2e-113;
Matches 909; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

26 CCGTGCCGCGCAGAGCGCTGCGATGCTGAGAGTTGCTGAGCGGAGCGGCTGCATCTG 85
Db      |||||
34 CTGATACCGGCGCGAATTCGCGGATGAGAGTTGCGAGCCGAGCGAGCTGATCCG 93
Qy      |||||
86 CGCCGCGTGCACCCCGCTGCTGAGAGCGGATCTGCGCGTCCCGAGAGCCCTCGAG 145
Db      |||||
94 CGCCGCGTGCACCCCGCTGCTGAGAGCGGATCTGCGCGTCCCGAGAGCCCTCGAG 153
Qy      |||||
146 GCCCGCGTGAAGCCCGGATCACTTCTCCCTGTGACCAACCGAGCGCTGAGAGTCC 205
Db      |||||
154 GCCCGCGTGAAGCCCGGATCACTTCTCCCTGTGACCAACCGAGCGCTGAGAGTCC 213
Qy      |||||
206 TGGCAATGCCGTTTGGGTGTGATCTTGGGCGCAAGAGAACTTAACCGCCATCCG 265
Db      |||||
214 TGGCAATGCCGTTTGGGTGTGATCTTGGGCGCAAGAGAACTTAACCGCCATCCG 273
Qy      |||||
266 AGGTGACTGACAGATATGATTTGGGACAGGTCAATCAAGACTGAGAGTTTGAATCT 325
Db      |||||
274 AGGTGACTGACAGATATGATTTGGGACAGGTCAATCAAGACTGAGAGTTTGAATCT 333
Qy      |||||
326 TCCGGGCGCAAGAGCAAGACGACAGGAGCTGACACTTCAAGAAATTCAGAGCGG 385
Db      |||||
334 TCCGGGCGCAAGAGCAAGACGACAGGAGCTGACACTTCAAGAAATTCAGAGCGG 393
Qy      |||||
386 ACCGCGCGAAGGTGCGGAAAGCTGCCAAGACGAGATAGCATCTCAAGATGTGAGC 445
Db      |||||
394 ACCGCGCGAAGGTGCGGAAAGCTGCCAAGACGAGATAGCATCTCAAGATGTGAGC 453
Qy      |||||
446 ATCCCAATCCTCTACAGCTGTGTGATGTTTGGACCCGCAAGAGTCTTATCTCC 505
Db      |||||
454 ATCCCAATCCTCTACAGCTGTGTGATGTTTGGACCCGCAAGAGTCTTATCTCC 513
Qy      |||||
506 TGGAGCTGCGCAGCGGAGAGGATGTTGATCTGATCTCTGACACAGGCTACTACTCG 565
Db      |||||
514 TGGAGCTGCGCAGCGGAGAGGATGTTGATCTGATCTCTGACACAGGCTACTACTCG 573
Qy      |||||
566 AGCGAGACAGAGCAAGCTGTGACCGCAAGTCTGTGAGGCGGCTATTTGACTCTAC 625
Db      |||||
574 AGCGAGACAGAGCAAGCTGTGACCGCAAGTCTGTGAGGCGGCTATTTGACTCTAC 633
Qy      |||||
626 TCAAGATCTGACAGAGATCTCAAGTGTGAGAACTGTGTTCTACACCGGCTGAGAA 685
Db      |||||
634 TCAAGATCTGACAGAGATCTCAAGTGTGAGAACTGTGTTCTACACCGGCTGAGAA 693
Qy      |||||
686 ACTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 745
Db      |||||
694 ACTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 753
Qy      |||||
746 AGCCCTGTGGAGCCCGGATATCTGCGCCAGAGGTGTAGGCGCGACGCGATAGAC 805
Db      |||||
754 AGCCCTGTGGAGCCCGGATATCTGCGCCAGAGGTGTAGGCGCGACGCGATAGAC 813
Qy      |||||
806 GCCCTGTGAGCTGTGGGCAATTTGAGTCAATGATCAATCTGCTTTCAGGCAATCAC 865
Db      |||||
814 GCCCTGTGAGCTGTGGGCAATTTGAGTCAATGATCAATCTGCTTTCAGGCAATCAC 873
Qy      |||||
866 CTTTCTATGAGAGAGTGAAGAGATATATATAGAACATATAGAAATCTCTCCGCA 925
Db      |||||
874 CTTTCTATGAGAGAGTGAAGAGATATATATAGAACATATAGAAATCTCTCCGCA 933
Qy      |||||
926 AGATCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 956
Db      |||||
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RESULT 13
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 LOCUS BX353478 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC006DP08 3-PRIME, mRNA sequence.
 ACCESSION BX353478
 VERSION BX353478.1 GI:30371769
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 911)
 Li W.B., Gruber C., Jessee J. and Polayes D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1934.r For more information about this cluster, see
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC006DH04NP1&cluster=1934.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC006DH04NP1.
 Location/Qualifiers
 source 1..911
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC006DP08"
 /issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 28.7%; Score 896.8; DB 13; Length 911;
 Best Local Similarity 99.3%; Pzed. No. 3e-112;
 Matches 906; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

208 CCACACTCTCCCGAGGCGCTTAACCTTGGGCGGCTTGGCTGAGAGCTGCTCCAGCGCA 2147
 911 CCACACTCTCCCGAGGCGCTTAACCTTGGGCGGCTTGGCTGAGAGCTGCTCCAGCGCA 852

2148 GGGCGCTGTCAGCGGCTCTTAGAGCTCCGACATGAGGTGTCCTGTGTGTGGGCT 2207
 851 GGGCGCTGTCAGCGGCTCTTAGAGCTCCGACATGAGGTGTCCTGTGTGTGGGCT 792

2208 GCTCTAGAGACAGATACAGGCTGTATAGAGATGAGAGGAGGAGGAGTATGTTTAA 2267
 791 GCTCTAGAGACAGATACAGGCTGTATAGAGATGAGAGGAGGAGTATGTTTAA 732

2268 GTCACAGCTTGGCAGCATGCTAGGAGTACTGCTACAGTGTGAGGCTCTCAGAGAGT 2327
 731 GTCACAGCTTGGCAGCATGCTAGGAGTACTGCTACAGTGTGAGGCTCTCAGAGAGT 672

2328 GAGAGAGTGTAGGAGGAGGAGAGAGCTTCATTTTGTCTTCTTAAGACCCGTATATT 2387
 671 GAGAGAGTGTAGGAGGAGGAGAGAGCTTCATTTTGTCTTCTTAAGACCCGTATATT 612

2388 GTGTATTTTCTCTCTTCCGAGTCTGACAGTGGGCTGACCTTACCCGAACTTCATGA 2447
 611 GTGTATTTTCTCTCTTCCGAGTCTGACAGTGGGCTGACCTTACCCGAACTTCATGA 552

2448 GCCTTAAGGAGAGAGAGCAATTAGGAGCTGTGCAATGAGACTGTGAGGCAAGATA 2507

DB 551 GCCTTAAGGAGAGAGAGCAATTAGGAGCTGTGCAATGAGACTGTGAGGCAAGATA 492

2508 CAAGCCGACACCCAGTGTCCAGGCTTAAGGAGTGTCTTACCTGGGCAACAGGAGG 2567
 491 CAAGCCGACACCCAGTGTCCAGGCTTAAGGAGTGTCTTACCTGGGCAACAGGAGG 432

2568 GCTGATACCTCTTCTCTCTCTAGATGCCACCTCTTACATCTCAGCCCAAGAGTCT 2627
 431 GCTGATACCTCTTCTCTCTCTAGATGCCACCTCTTACATCTCAGCCCAAGAGTCT 372

2628 CTCACACCTTGGGAGGCTTGTGTCATGAGCAATGAGCAATGAGTGTGAGGTTTGGCC 2687
 371 CTCACACCTTGGGAGGCTTGTGTCATGAGCAATGAGCAATGAGTGTGAGGTTTGGCC 312

2688 TTTACAGGGGAGATTTTCTGTCATGTTCAACATGAAATGAGAGAACTTCTCTTTC 2747
 311 TTTACAGGGGAGATTTTCTGTCATGTTCAACATGAAATGAGAGAACTTCTCTTTC 252

2748 TACAGCTACTTCTATACAGAGGCGCAGGTCGCTAGAGCCCAATTGCTTTTCTG 2807
 251 TACAGCTACTTCTATACAGAGGCGCAGGTCGCTAGAGCCCAATTGCTTTTCTG 192

2808 GGATAGAGAGATGAGGTTAACTCCCACTTCTGAGGAGGCTCTGACAGAGTCCCT 2867
 191 GGATAGAGAGATGAGGTTAACTCCCACTTCTGAGGAGGCTCTGACAGAGTCCCT 132

2868 TTGTACAGACCTTACACAGCCTGATGAGCAAGCAATGAGTCTGCTGCTGCTGCGCA 2927
 131 TTGTACAGACCTTACACAGCCTGATGAGCAAGCAATGAGTCTGCTGCTGCTGCGG-A 73

2928 CTCCTGTGTGCTCTGCTGCTTCTCCCTGACATGCTGTGAGTCTGCTGTGTAAGG 2987
 72 CTCCTGTGTGCTCTGCTGCTTCTCCCTGACATGCTGTGAGTCTGCTGTGTAAGG 13

2988 TCGGTGGGTTAA 2999
 12 TCGGTGGGTTAA 1

DB 12 TCGGTGGGTTAA 1

RESULT 14
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 LOCUS BX353479 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC006DP08 5-PRIME, mRNA sequence.
 ACCESSION BX353479
 VERSION BX353479.1 GI:30373761
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 955)
 Li W.B., Gruber C., Jessee J. and Polayes D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1934.r For more information about this cluster, see
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC006DH04NP1&cluster=1934.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC006DH04NP1.
 Location/Qualifiers
 source 1..955
 /organism="Homo sapiens"
 /mol_type="mRNA"
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/clone="CS0DC0061P08"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cdna was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cdna was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN
Query Match      28.0%; Score 875.4; DB 13; Length 955;
Best Local Similarity 96.5%; Pred. No. 2.4e-109;
Matches 864; Conservative 25; Mismatches 6; Indels 0; Gaps 0;

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61 CGGAGATGTTGCTAGCCGAGCGCGCTGCTATGCGCCGCTCTGCTGCTGCTGCTGCA 120
112 GCGGATTTGCTGCGCGCGCTGCTGCGAGCCCTGCGCGCGCTGCTGCGCGCTGCTGCA 171
121 GCGGATTTGCTGCGCGCGCTGCTGCGAGCCCTGCGCGCGCTGCTGCGCGCTGCTGCA 180
172 TCCCTGTGACCAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 231
181 TCCCTGTGACCAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
232 CTGAGCGCAAGAGAGATATATACCAAGCCATCGAGAGTGAATGATATATATATATAT 291
241 CTGAGCGCAAGAGAGATATATACCAAGCCATCGAGAGTGAATGATATATATATATAT 300
292 CAGGTATCATCAAGCTGAGAGATTTGTGTAATCTTCCGCGCGCAAGAGAGAGAGAG 351
301 CAGGTATCATCAAGCTGAGAGATTTGTGTAATCTTCCGCGCGCAAGAGAGAGAGAG 360
352 AAGCTGCAACCTGCGCAAGAGTTTCCAGAGCGGAGCGCGCAAGAGTGGGAAAGCTGCC 411
361 AAGCTGCAACCTGCGCAAGAGTTTCCAGAGCGGAGCGCGCAAGAGTGGGAAAGCTGCC 420
412 AAGAGAGAGATGAGCTCTCTCAAGATGAGAGAGATCCCAATCTTCAAGCTGCTGAT 471
421 AAGAGAGAGATGAGCTCTCTCAAGATGAGAGAGATCCCAATCTTCAAGCTGCTGAT 480
472 GGTGTTGTAACCGCGAGAGATATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
481 GGTGTTGTAACCGCGAGAGATATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
532 TTTGACTGATCTGAGACGAGGCTACTACTCGAGACGAGACAGACAGCAACGCTGTACGG 591
541 TTTGACTGATCTGAGACGAGGCTACTACTCGAGACGAGACAGACAGCAACGCTGTACGG 600
592 CAGGTCTGAGAGCGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
601 CAGGTCTGAGAGCGCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
652 CTGAGAGAGCTGTTACTACAACCGCGTGAAGAACTCGAAGATTGTCATGCTGACTGCT 711
661 CTGAGAGAGCTGTTACTACAACCGCGTGAAGAACTCGAAGATTGTCATGCTGACTGCT 720
712 CATCTGCTAGCTAGAAAAATGCTCATCAAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCT 771
721 CATCTGCTAGCTAGAAAAATGCTCATCAAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCT 780
772 GCCCAAGAGTGTAGAGCGCGAGCGGATATGACGCGCTGCTGCTGCTGCTGCTGCTGCT 831
781 GCCCAAGAGTGTAGAGCGCGAGCGGATATGACGCGCTGCTGCTGCTGCTGCTGCTGCT 840
832 GTCATATATGATACCTGCTTCTGAGGATCCACTTTCTATGAGAGAGTGAAGAAGAT 891
841 GTCATATATGATACCTGCTTCTGAGGATCCACTTTCTATGAGAGAGTGAAGAAGAT 900
892 GATTATGAGAACCATTAAGAAATCTCTCCGAGAGATCTGCTGCTGCTGCTGCTGCTGCT 946
901 AATTATGAGAACCATTAAGAAATCTCTCCGAGAGATCTGCTGCTGCTGCTGCTGCTGCT 955

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RESULT 15
BX423239/c 1201 bp mRNA linear EST 15-MAY-2003
LOCUS BX423239 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF003YA22 3-PRIME, mRNA sequence.
ACCESSION BX423239.1 GI:30766248
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1934.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AF001ZE1NP1&cluster=1934.r. Contact :
Peng Liang Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF001ZE1NP1.
Location/Qualifiers

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FEATURES

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/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cdna
was primed with a NotI-oligo (dt) primer. Five prime end
enriched, double-strand cdna was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

ORIGIN

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Query Match      27.8%; Score 867.6; DB 13; Length 1201;
Best Local Similarity 89.2%; Pred. No. 2.5e-108;
Matches 928; Conservative 17; Mismatches 92; Indels 3; Gaps 3;
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1038 TGKGGGAGAGCGCTCWAAGAACTCAGGGGCGCCKGCTCTCTCCCTCCCTCCCTCTGTCG 979
2056 CTCACATCTCCCTC-AGCGAGCGCTGCAAGTCCCACTCTCTCCAGGCCCTAACTGG 2114
978 CKACCAATCCCTGAGAGCGGCGCTGCAKCCCACTCTCTCCAGGCCCTAATCTGG 919
2115 GCGGCTTGGCCTGAGAGCTGATCTTCCAGCGAGGCGCTGTCAGCGTCTTAACTCTCG 2174
918 GCGGCTTGGCCTGAGAGCTGATCTTCCAGCGAGGCGCTGTCAGCGTCTTAACTCTCG 859
2175 CACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2234
858 CACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 799
2235 AGAGAGTGAAGAGTGAAGGAGATGTTAATGTCAGACTTGAGCATGAGGATGAGGAT 2294
798 AGAGAGTGAAGAGTGAAGGAGATGTTAATGTCAGACTTGAGCATGAGGATGAGGAT 739
2295 ACTGCTAGTACTGTGAGAGTCTCTCAGAGTGAAGAGATGAGTGAAGAGGAGAGAGCT 2354
738 ACTGCTAGTACTGTGAGAGTCTCTCAGAGTGAAGAGATGAGTGAAGAGGAGAGAGCT 679

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QY 2355 TCATTTTGTCTCTCTAAGACCTGTATTGTATTCTGCTTCCAGTCT 2414
DB 678 TCCATTTTGTCTCTCTAAGACCTGTATTANNGGTANNCCGCGAGGCC- 620
QY 2415 GCAGTGGGCTCCCTGTACCTGTAACTCATAGCCTTAAGGAAAGAGAACAATTA 2474
DB 619 GCAGTGGGCTCCCTGTACCTGTAACTCATAGCCTTAAGGAAAGAGAACAATTA 560
QY 2475 GGAGTGGCAATGAGACTGGCAGGCGAGATCAAGCCAGCACCAAGTGTCCAGCT 2534
DB 559 GGAGGAGCAAGAGACTGGCAGGCGAGAGACAGCACCAAGCGGCCAGCCN 500
QY 2535 TACTGAGTCTTACCTGGGCGAAAGAGGAGGCTGATACCTCTGCTCTCTAGAT 2594
DB 499 AACGGGGGCTAAACCCGGGCGAAAGAGGAGGCGATACCCCTGCTTCCAGAT 440
QY 2595 GCCGACTCTCTACATCTCAGCCCAAGATCTCTCCACCTTAGGGGCTTGTGCATGG 2654
DB 439 GCCCACCCCGACATCCGAGCCCAAGACCCCCGACCTTAGGGGCTTGTGCATGG 380
QY 2655 CAATPACTCATATCTGATTGTGAGGTTTGCCTTTACAGGGCGAGATTTTGTGCTAGT 2714
DB 379 CAAAACCCCAAAATCGATGAGAGGTTGCGCTTAAAGGGCGAGATTTTGTGCTAGT 320
QY 2715 TCAACAAATGAATGAAGAGAACTCCCTCTTTTACAGCTCACTTATCAGAGGCCAG 2774
DB 319 TCAACAAATGAATGAAGAGAACTCCCTCTTTTCAAGCTCACTTATCAGAGGCCAG 260
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DB 259 GTGCTCAGAGCCACATTGAGTTGCTTTTCTGGAGAGGAGTAGGGTTAACTCCC 200
QY 2835 AGTTTCTGAGGAGGCTCTGACAGGTGCCCTTTGTACAGACCTTACACAGCCTGATA 2894
DB 199 AGTTTCTGAGGAGGCTCTGACAGGCGCCCTTTGTACAGACCTTACACAGCCTGATA 140
QY 2895 GGCAGCCACATTGCTCTCGCCCTTGTCTGCGACTCCGTGTGCTCTGCTTCTGCT 2954
DB 139 GGCAGCCACATTGCTCTCGCCCTTGTCTGCGG-ACITCGTGTGCTCTGCTTCTGCT 81
QY 2955 GCATGCTGTGGGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 3014
DB 80 GCATGCGCNGNGGNCNGCNGGNGGAGAGNGGAGGNGNNAACAGNGNGCCNACTGA 21
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DB 20 ACCGGGCAAAATAACACAC 1
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Search completed: April 27, 2004, 05:11:42
Job time : 7638 secs

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DB 301 AAGACTGAGAGTCTTTTGTGAAATCTTCCGGGCGAAGGACGACAGGCAAGCTGCAC 360
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DB 361 AACTGCAGAAAGTTCACAGAGGGGAGCGGCGCCAGAGGTGCCGAAAGCTCCAGAAACGAG 420
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DB 421 ATAGGCACTCTCAAGTGTGAGCATCCCAACATCTCTACAGCTGTGAGATGTGTTGTG 480
QY 481 ACCCGAGAGAGTACTTTATCTTCTGAGACTGGCCACGGGAGGGAGGTTGTTGAC 540
DB 481 ACCCGAGAGAGTACTTTATCTTCTGAGACTGGCCACGGGAGGGAGGTTGTTGAC 540
QY 541 ATCTTGACACAGGGCTACTACTGAGCGAGACACAGCAAGTGTGTACGGCAAGTCTG 600
DB 541 ATCTTGACACAGGGCTACTACTGAGCGAGACACAGCAAGTGTGTACGGCAAGTCTG 600
QY 601 GAGGCGGTGGCCATTTTGACCTCAAGATCTGACAGGAACTCTCAAGCTGAGAAC 660
DB 601 GAGGCGGTGGCCATTTTGACCTCAAGATCTGACAGGAACTCTCAAGCTGAGAAC 660
QY 661 CTGGTTTACTACACCGGCTGAAAGACTGGAAGATTGTCACTGATGACTTCCATCTGCT 720
DB 661 CTGGTTTACTACACCGGCTGAAAGACTGGAAGATTGTCACTGATGACTTCCATCTGCT 720
QY 721 AAGCTGAAAGATGGCTCTCAACAGAGCCCTGTGGACCCCGAGATCTGGCCCCAGAG 780
DB 721 AAGCTGAAAGATGGCTCTCAACAGAGCCCTGTGGACCCCGAGATCTGGCCCCAGAG 780
QY 781 GTGGTGGCGCGGAGCGGTATGACCGCTGTGTGACTGTGGGCAATGGAGTCACTATG 840
DB 781 GTGGTGGCGCGGAGCGGTATGACCGCTGTGTGACTGTGGGCAATGGAGTCACTATG 840
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QY 901 AACCATGATAGAAATCTCTTCGCGCAGATCTGCTGTGACTATGATGATTGACTCTCA 960
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QY 961 TATTGGAGTATTTTCGAGGCGACCCAAAGACTTGTCACAAGGCTGATGAGGTGGAG 1020
DB 961 TATTGGAGTATTTTCGAGGCGACCCAAAGACTTGTCACAAGGCTGATGAGGTGGAG 1020
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QY 1081 GCTTCTGATPAGAACTCAAGAGATGTGTCTGCGCCAGATTGAAAGAACTTTCAGAG 1140
DB 1081 GCTTCTGATPAGAACTCAAGAGATGTGTCTGCGCCAGATTGAAAGAACTTTCAGAG 1140
QY 1141 GCCCAAGTGAAGAGGCTGTCCGAGTGAACACCCCTCATGAAAAGGCTCCGGGACACAG 1200
DB 1141 GCCCAAGTGAAGAGGCTGTCCGAGTGAACACCCCTCATGAAAAGGCTCCGGGACACAG 1200
QY 1201 CAGTCCAGACGCGCTCAGCGCCAGTGGCTCAGCCACAGACATCTGCCACCCCGGGGCT 1260
DB 1201 CAGTCCAGACGCGCTCAGCGCCAGTGGCTCAGCCACAGACATCTGCCACCCCGGGGCT 1260
QY 1261 GCGAGTGGGGGCGACAGCTGAGCTGAGAGTGAAGTCAAGCCCTGAGAGGTATGCT 1320
DB 1261 GCGAGTGGGGGCGACAGCTGAGCTGAGAGTGAAGTCAAGCCCTGAGAGGTATGCT 1320
QY 1321 GCTCTGTCTCAAGAGTGAATATGTGGCCCCCGCAGACCTGATGTCCACCCACAGCACA 1380
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RESULT 2
US-10-153-921-1
Sequence 1, Application US/10153921
Patent No. 6653116

GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO0612DIV
CURRENT APPLICATION NUMBER: US/10153,921
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/207,281
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/734,030
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 1
LENGTH: 3124
TYPE: DNA
ORGANISM: HOMO SAPIEN
US-10-153-921-1

Query Match 100.0%; Score 3124; DB 4; Length 3124;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dymnac, Radoje T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ. ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ. ID NO 20
LENGTH: 2840
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (206)..(1711)
US-09-620-312D-20
Query Match 89.3%; Score 2791.2; DB 4; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 2385 GTTATTTCTGCTTCCAGAGTCTGCTGAGTGGAGTCCCTGATACCTGATACCTGATACCTGATAC 2444
QY 2450 CTCTAAAGGAGAGAGAGAGATTAAGAGCTGGCAATGAGACCTGGCAGGAGGAGGAGGAGGAGGAG 2509
DB 2445 CTCTAAAGGAGAGAGAGAGATTAAGAGCTGGCAATGAGACCTGGCAGGAGGAGGAGGAGGAGGAG 2504
QY 2510 AGCCGAGAGAGAGAGTCTGAGGCTTAACTGAGGCTTAACTGAGGCTTAACTGAGGCTTAACTGAG 2569
DB 2505 AGCCGAGAGAGAGAGTCTGAGGCTTAACTGAGGCTTAACTGAGGCTTAACTGAGGCTTAACTGAG 2564
QY 2570 TGAATCCTGCTGCTTCTAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2629
DB 2565 TGAATCCTGCTGCTTCTAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2624
QY 2630 CCAACCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2689
DB 2625 CCAACCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2684

QY 2690 TACAGGAGGAGATTTTCTGCTGATTCACAAATGAAATGAGAGGAGAACTCCCTCTTCTA 2749
DB 2685 TACAGGAGGAGATTTTCTGCTGATTCACAAATGAAATGAGAGGAGAACTCCCTCTTCTA 2744
QY 2750 CAGCTACCTCTATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2809
DB 2745 CAGCTACCTCTATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2804
QY 2810 ATGAGGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2845
DB 2805 ATGAGGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2840

RESULT 4
US-09-620-312D-19
Sequence 19, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 19
LENGTH: 2747
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (206) .. (1618)
US-09-620-312D-19

Query March 83.1k; Score 2595.2; DB 4; Length 2747;
Best Local Similarity 96.6k; Pred. No. 0;
Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;
QY 50 TGCTGAGAGTTCGCTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 109
DB 45 TGCTGAGAGTTCGCTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 104
QY 110 GAGCGGATTCGCGCGGCTTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 169
DB 105 GAGCGGATTCGCGCGGCTTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 164
QY 170 CCTGCTGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 229
DB 165 CCTGCTGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 224
QY 230 CTCGAGGAGCAGAGAGAGCTATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 289

Db	225	CTCTGGGGGACAAAGAACCTATTAACACGCCATGGAGGTGATCTGACAGATATATGATTGG	284
Qy	290	GACAGGTTCATCAAGACTGAGGAGTTTGTGAAATCTTCCGGGCCAAGACAGACGACG	349
Db	285	GACAGGTTCATCAAGACTGAGGAGTTTGTGAAATCTTCCGGGCCAAGACAGACGACG	344
Qy	350	GCAAGCTGCACACCTGSCAAGAAAGTTCCAGAACGGGGGACGGCCGGAAGTGGGAAACCTG	409
Db	345	GCAAGCTGCACACCTGSCAAGAAAGTTCCAGAACGGGGGACGGCCGGAAGTGGGAAACCTG	404
Qy	410	CCAAGAACGAGATAGGCATCTCTCAAGATGTGTGAAGACATCCCAACATCTCACTAGCTGTGG	469
Db	405	CCAAGAACGAGATAGGCATCTCTCAAGATGTGTGAAGACATCCCAACATCTCACTAGCTGTGG	464
Qy	470	ATGTGTTTGTGACCCGCAAGGAGTACTTTATCTTCTTGGAGCTGGCCACGGGAGGAGG	529
Db	465	ATGTGTTTGTGACCCGCAAGGAGTACTTTATCTTCTTGGAGCTGGCCACGGGAGGAGG	524
Qy	530	TGTTTGAATGATTCCTTGACCAAGGGCTATCTGTGGAGCCGAGACACAAAGCAACTGTGTAC	589
Db	525	TGTTTGAATGATTCCTTGACCAAGGGCTATCTGTGGAGCCGAGACCAAGCAACTGTGTAC	584
Qy	590	GCGAAGTCTGTGAGGCGGTGGCTTATTTGGCACTACCTCAATGATGTGACAGAAATCTCA	649
Db	585	GCGAAGTCTGTGAGGCGGTGGCTTATTTGGCACTACCTCAATGATGTGACAGAAATCTCA	644
Qy	650	AGCTGGAGAACCTGTGTTACTACCAACCGGCTGAAGAACTCGAAGATTGTCACTAGTACT	709
Db	645	AGCTGGAGAACCTGTGTTACTACCAACCGGCTGAAGAACTCGAAGATTGTCACTAGTACT	704
Qy	710	TCCATCTGGCTAAGCTAGAAAATGGCCTCATCAAGAGACCTGTGGGACCCCGCAGTATC	769
Db	705	TCCATCTGGCTAAGCTAGAAAATGGCCTCATCAAGAGACCTGTGGGACCCCGCAGTATC	764
Qy	770	TGGCCCCAGAGGTGGTAGCCGGGACGGGTATGAGCGCCGTGTGGAATGCTGTGGGCAATTG	829
Db	765	TGGCCCCAGAGGTGGTAGCCGGGACGGGTATGAGCGCCGTGTGGAATGCTGTGGGCAATTG	824
Qy	830	GAGTCATCATATACATCCTGTCTTCAGGCAATCCACCTTTCTATGAGGAGGTGGAAGAG	889
Db	825	GAGTCATCATATACATCCTGTCTTCAGGCAATCCACCTTTCTATGAGGAGGTGGAAGAG	884
Qy	890	ATGATTTATGAGAACCATATGATAAGAACTCTTCCGCAAGATCTTGGCTGTGATATGAGT	949
Db	885	ATGATTTATGAGAACCATATGATAAGAACTCTTCCGCAAGATCTTGGCTGTGATATGAGT	944
Qy	950	TTGATCTCCCATATTGGGATGTATATTGGGACGACGCCAAGAACCTGGTCCAMAGGCTGA	1009
Db	945	TTGATCTCCCATATTGGGATGTATATTGGGACGACGCCAAGAACCTGGTCCAMAGGCTGA	1004
Qy	1010	TGAGAGTGGACCAAGACCAAGCGSAGTCACTGACAGAAAGAGCCCATCTCCCATAGTGAATTT	1069
Db	1005	TGAGAGTGGACCAAGACCAAGCGSAGTCACTGACAGAAAGAGCCCATCTCCCATAGTGAATTT	1064
Qy	1070	CTGGCAATGTGCTTTCTGATTAAGAACATCAAGATGATGTCTGTGGCCCAATTGAATAA	1129
Db	1065	CTGGCAATGTGCTTTCTGATTAAGAACATCAAGATGATGTCTGTGGCCCAATTGAATAA	1124
Qy	1130	ACTTTTGGCCAGGGCCCAAGTGAAGAAAGGCTGTTCGAGTGAACCACTCTATGAAAAGGCTCC	1189
Db	1125	ACTTTTGGCCAGGGCCCAAGTGAAGAAAGGCTGTTCGAGTGAACCACTCTATGAAAAGGCTCC	1184
Qy	1190	GAGGACCAAGAGAGTCCAGACACGGGTGACGCCAGTGGGCTCAAGCCACAGACACTGGCA	1249
Db	1185	GAGGACCAAGAGAGTCCAGACACGGGTGACGCCAGTGGGCTCAAGCCACAGACACTGGCA	1244
Qy	1250	CCCCCGGGGCTGCAGGTGGGGGCAACAGCTGACGTGCGAGTGAAGTCACTCAAGCCCTCG	1309
Db	1245	CCCCCGGGGCT-----	1255
Qy	1310	AGGGTGAATGCTGCTGTGTGCTGCAAAAGATGATATGTGGCCCCCGCAGACCTGTATGTCCA	1369
Db	1256	-----GCAACACGATGATGTCCA	1271

QY	1370	CCCCAGCCACAGATGGAAATGGTCCACCCCAACCACTGTATGGCAATGTTCACCCCAAGCCACCG	1423
Db	1272	CCCCAGCCACAGATGGAAATGGTCCACCCCAACCACTGTATGGCAATGTTCACCCCAAGCCACCG	1331
QY	1430	ATGGAAAGCATCACTCCAGCCACTGTATGGAGATGTCAACCCAGATCACTGAAGAGAGCCTA	1489
Db	1332	ATGGAAAGCATCACTCCAGCCACTGTATGGAGATGTCAACCCAGAGCTACTGAAGAGAGCCTA	1391
QY	1490	CTCCAGCCACTGTATGGAGAGCCACACAGCCACAGAAAGAGACACTGTGCCACACACC	1549
Db	1392	CTCCATCTCACTGTATGGAGTAGCCACACAGCCACAGAAAGAGACACTGTGCCACACACC	1451
QY	1550	AAAGCACTGCTCATGTCTGGCCACCAAGGCACTGCCACCCCTGAGCCGGCTATGGCCAGC	1609
Db	1452	AAAGCACTGCTCATGTCTGGCCACCAAGGCACTGCCACCCCTGAGCCGGCTATGGCCAGC	1511
QY	1610	CGGACAGCACAGCCCCAGAGAGGGGCCACAGGCCAGGTCCACCCCTCTAATGAAGGGGAAG	1669
Db	1512	CGGACAGCACAGCCCCAGAGAGGGGCCACAGGCCAGGTCTCACCCCTCTAATGAAGGGGAAG	1571
QY	1670	AGGCTGTGCTTTATGCCAGAGATCTCAAGGGAGAGGAGGCACTGTATGGAGCAAGCCTGG	1729
Db	1572	AGGCTGTGCTTTATGCCAGAGATCTCAAGGGAGAGGAGGCACTGTATGGAGCAAGCCTGG	1631
QY	1730	TGAGGGGGGGCAGAGGGATGGGGCAGAGAGGTGGGAGATGATAGGGGGCTTCTCACTGTA	1789
Db	1632	TGAGGGGGGGCAGAGGGATGGGGCAGAGAGGTGGGAGATGATAGGGGGCTTCTCACTGTA	1691
QY	1790	CATAGACTCACTGGCATGATGATCCCTGCTCCGCCATGCCCCCAATCCAGTGGGGGATA	1849
Db	1692	CATAGACTCACTGGCATGATGATCCCTGCTCCGCCATGCCCCCAATCCAGTGGGGGATA	1751
QY	1850	ACTAGGGGGTCACGGAGAGACAGTCTGCTCTCTGTGTGTATGTGTGTGAATGCTGGGAG	1909
Db	1752	ACTAGGGGGTCACGGAGAGACAGTCTGCTCTCTGTGTGTGTGTGTGAATGCTGGGAG	1811
QY	1910	GCCAGTGGCAGGGGCCGAGCCCAAGCCCTGGATGGAATCCCTGTGGCTTTCGTCTTTG	1969
Db	1812	GCCAGTGGCAGGGGCCGAGCCCAAGCCCTGGATGGAATCCCTGTGGCTTTCGTCTTTG	1871
QY	1970	CTAGCTTCAACAAGTTTGTGTCTTGTGGAGATCTGCTCTAGAGGATACTCAGAGGAGCTCC	2029
Db	1872	CTAGCTTCAACAAGTTTGTGTCTTGTGGAGATCTGCTCTAGAGGATACTCAGAGGAGCTCC	1931
QY	2030	TGCTCTCTCTCCCTTCCCTTCTTCTCTCAACAATCCCTAGGCAAGGCCCTGCAAGTCCC	2089
Db	1932	TGCTCTCTCTCCCTTCCCTTCTTCTCTCAACAATCCCTAGGCAAGGCCCTGCAAGTCCC	1991
QY	2090	ACACTCTCCAGAGCCCTAAACTTGGGGGAGCTTGGCCCTGAGAGGTGGTCTCCAGCAGG	2149
Db	1992	ACACTCTCCAGAGCCCTAAACTTGGGGGAGCTTGGCCCTGAGAGGTGGTCTCCAGCAGG	2051
QY	2150	CCCTGTAGAGGCTTTAAGGCTCCGTCACATGAAGAGTGTGGCCGTGGTGTGGTGGCTGC	2209
Db	2052	CCCTGTAGAGGCTTTAAGGCTCCGTCACATGAAGAGTGTGGCCGTGGTGTGGTGGCTGC	2111
QY	2210	TCTAGAGCAGATTCACAGGCTGTTATAGAGATGCAGAAAGTATGGGCAATATGTTTAAGT	2269
Db	2112	TCTAGAGCAGATTCACAGGCTGTTATAGAGATGCAGAAAGTATGGGCAATATGTTTAAGT	2171
QY	2270	CCAGACTTGGCACAATGGCTTAGGATTAAGTCTCACTAGCTGTGGAGGTCTCAAGAGTGA	2329
Db	2172	CCAGACTTGGCACAATGGCTTAGGATTAAGTCTCACTAGCTGTGGAGGTCTCAAGAGTGA	2231
QY	2330	GAGAGATGATAGAGAGGCGAAGACTTCAATTTTGTCTCTTAAGACCTCTGTATTTGT	2389
Db	2232	GAGAGATGATAGAGAGGCGAAGACTTCAATTTTGTCTCTTAAGACCTCTGTATTTGT	2291
QY	2390	GTTATTTTCAGGCTTTCGAGAGTCTCTGAGAGGGGTGCGCTGATCCCGAAGCTCATAGC	2449
Db	2292	GTTATTTTCAGGCTTTCGAGAGTCTCTGAGAGGGGTGCGCTGATCCCGAAGCTCATAGC	2351

QY	2450	TTCTTAAGGGAAGGAGGAACAATTATGACAGTGGCAATGAGACTCTGGGCGACAGTACA	2509
Db	2352	CTCTTAAGGGAAGGAGGAACAATTATGACAGTGGCAATGAGACTCTGGGCGACAGTACA	2411
QY	2510	AGCCGAGCACCCAGTGTCCCAAGCCTTAATGGAGTCTTACCTCTGGGCCAAACAGGAGAGGC	2569
Db	2412	AGCCGAGCACCCAGTGTCCCAAGCCTTAATGGAGTCTTACCTCTGGGCCAAACAGGAGAGGC	2471
QY	2570	TGATACCTCTTGTCTCTTCTAGATGCGCCACCTCTCAATCTCAGCCACAGAATCTCT	2629
Db	2472	TGATACCTCTTGTCTCTTCTAGATGCGCCACCTCTCAATCTCAGCCACAGAATCTCT	2531
QY	2630	CCACCCTAAGGGGGCTTGTGTCATGGGCATTAATCTCAATCTGATTTGAGGTTGGCCCTT	2689
Db	2532	CCACCCTAAGGGGGCTTGTGTCATGGGCATTAATCTCAATCTGATTTGAGGTTGGCCCTT	2591
QY	2690	TACAGGGGCAGATTTTCTGCTCAGTTCACAATGAATGAAGAGAACTCCCTCTTCTA	2749
Db	2592	TACAGGGGCAGATTTTCTGCTCAGTTCACAATGAATGAAGAGAACTCCCTCTTCTA	2651
QY	2750	CAGCTCACTTCTATCAGAGGCCCAAGTSCCTCAGAGCCACAATTGAGTTGCTTTTCTGGG	2809
Db	2652	CAGCTCACTTCTATCAGAGGCCCAAGTSCCTCAGAGCCACAATTGAGTTGCTTTTCTGGG	2711
QY	2810	ATGAGGAAGTAGGGTTAAATCTCCCAAGTTTCTGAG	2845
Db	2712	ATGAGGAAGTAGGGTTAAATCTCCCAAGTTTCTGAG	2747

RESULT 5
TIS-09-73

```

; Sequence 3, Application US/09734030
; Patent No. 6461846
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M.
; APPLICANT: MERKLOV, Genady
; APPLICANT: KETCHUM, Karen A.
; APPLICANT: WEI, Ming-Hui
; APPLICANT: DIPRANCESCO, Valentina
; APPLICANT: YAN, Chunhua
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000612
; CURRENT APPLICATION NUMBER: US/09/734,030
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7542
; TYPE: DNA
; ORGANISM: HUMAN
US-09-734-030-3

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Query Match	60.1%;	Score 1876.6;	DB 4;	Length 7542;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1890; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1;

QY	1151	AGAAAGCTGTCCGAGTGACCACTCTATGAAAAGGCTCCGGGCAACAGCAGTCACGCA	1210
Db	3979	AGAAAGCTGTCCGAGTGACCACTCTATGAAAAGGCTCCGGGCAACAGCAGTCACGCA	4038
QY	1211	CGGCTGCAGAGCCAGTCGGGCTCAGGACACAGAACTGACACCCCGGGGGTGAAGTGGGG	1270
Db	4039	CGGCTGCAGAGCCAGTCGGGCTCAGGACACAGAACTGACACCCCGGGGGTGAAGTGGGG	4099
QY	1271	CCACAGCTCAGACTGCGAGTGAGCTCACTCAGCCCTGAGGGTGAATGCTGCTCGTGCTG	1330
Db	4099	CCACAGCTCAGACTGCGAGTGAGCTCACTCAGCCCTGAGGGTGAATGCTGCTCGTGCTG	4159
QY	1331	CAAAAGATATATGTGGCCCCCGCAGACCTGTAATGTGCCACCCCAAGCACAAGATGGAAGTG	1390

[illegible]

Db 5239 TCCTGACATGAGGAGCCCTGTAACCTGAACTCATGAGCTCTTAAGGAAAGAGAAACA 5298
QY 2411 ATTAGAGAGTGGCAATGAGACCTGGCAGAGGAGAGTACAGCCAGCAACCCAGTGTCCCA 2530
Db 5289 ATTAGAGAGTGGCAATGAGACCTGGCAGAGGAGAGTACAGCCAGCAACCCAGTGTCCCA 5358
QY 2511 GCGTTACTGGGGTCCCTTAACCTGGGCGAAACAGGAGGGGTATATCTCTTGTCTTCTT 2590
Db 5359 GCGTTAATGGGTCTTACCAATGAGGCGAAACAGGAGGGGTATATCTCTTGTCTTCTTCT 5418
QY 2591 AGATGCCACCTCTCTCAATCATCTCAGCCCAAGTCTCTTCCACCTTAGGGGGCTTGTGTC 2650
Db 5419 AGATGCCACCTCTCTCAATCATCTCAGCCCAAGTCTCTTCCCA-CCTAGGGGGCTTGTGTC 5477
QY 2651 ATGGCAATTAATCATTAATCTGATTTGAGGTTTGGCCCTTTACAGGGGAGATTTTGTGCT 2710
Db 5478 ATGGCAATTAATCATTAATTTGAGGTTTGGCCCTTTACAGGGGAGATTTTGTGCT 5537
QY 2711 CAGTTCAACATGAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTCTATCAGAGGC 2770
Db 5538 CAGTTCAACATGAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTCTATCAGAGGC 5597
QY 2771 CCAGTGGCTCAGAGCCCATTTGAGTTGCTTTTCTGGGATGAGGAGTAACT 2830
Db 5598 CCAGTGGCTCAGAGCCCATTTGAGTTGCTTTTCTGGGATGAGGAGTAACT 5657
QY 2831 CCCCAGTTCTCTGAGGAGGCTCTCTGACAGGTGCTCTTGTGACACCTTACACAGGCTG 2890
Db 5658 CCCCAGTTCTCTGAGGAGGCTCTCTGACAGGTGCTCTTGTGACACCTTACACAGGCTG 5717
QY 2891 GATAGGAGCCACATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
Db 5718 GATAGGAGCCACATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5777
QY 2951 CCGTGCATGCTGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010
Db 5778 CCGTGCATGCTGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5837
QY 3011 CTGAACCTGGCAATTAACATCACTCCCTGCAAGGC 3045
Db 5838 CTGAACCTGGCAATTAACATCACTCCCTGCAAGGC 5872

RESULT 6

US-10-153-921-3
Sequence 3, Application US/10153921

Patent No. 6653116

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CLO00612DIV

CURRENT FILING DATE: US/10/153,921

PRIOR FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/207,281

PRIOR FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 09/734,030

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 7542

TYPE: DNA

ORGANISM: HOMO SAPIEN

US-10-153-921-3

Query Match 60.1%; Score 1876.6; DB 4; Length 7542;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1151 AGAAGCTGTCCGAGTACCACTCATGAACGGCTCCGGGACCAAGAGATCCAGCA 1210

Db 3979 AGAAGCTGTCCGAGTACCACTCATGAACGGCTCCGGGACCAAGAGATCCAGCA 4038
QY 1211 CGGCTCAGCCAGTGGGCTTACGACCAAGAGACTGCAACCCCGGGGCTGAGTGGG 1270
Db 4039 CGGCTCAGCCAGTGGGCTTACGACCAAGAGACTGCAACCCCGGGGCTGAGTGGG 4098
QY 1271 CCAAGCTGAGTGGGAGTGAAGTCACTCAGCCCTGAGGGGTAGTGTCTGCTG 1330
Db 4099 CCAAGCTGAGTGGGAGTGAAGTCACTCAGCCCTGAGGGGTAGTGTCTGCTGCTG 4158
QY 1331 CAAAGGTATATGTGGGCCCCCGAGACCGTATGTCACCCAGCAAGATGGAAGT 1390
Db 4159 CAAAGGTATATGTGGGCCCCCGAGACCGTATGTCACCCAGCAAGATGGAAGT 4218
QY 1391 CCAACCCAGCCACTGATGAGTGAACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1450
Db 4219 CCAACCCAGCCACTGATGAGTGAACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 4278
QY 1451 CTGATGAGAGTGTCAACCCAGTCACTGACAGAGGCTACTCAGGCACTGATGAGAG 1510
Db 4279 CTGATGAGAGTGTCAACCCAGTCACTGACAGAGGCTACTCAGGCACTGATGAGAG 4338
QY 1511 CCAACACACCCAG 1570
Db 4339 CCAACACACCCAG 4398
QY 1571 CCAAGGAGAGTGCACCCCTGAGCCGGGCTATGGCCAGCCGAGAGAGAGAGAGAGAG 1630
Db 4399 CCAAGGAGAGTGCACCCCTGAGCCGGGCTATGGCCAGCCGAGAGAGAGAGAGAGAG 4458
QY 1631 GCGCCACAGGAGAGTCCACCTCTAGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
Db 4459 GCGCCACAGGAGAGTCCACCTCTAGTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 4518
QY 1691 AGTCTCAAAGGAG 1750
Db 4519 AGTCTCAAAGGAG 4578
QY 1751 CAGAGAGGAG 1810
Db 4579 CAGAGAGGAG 4638
QY 1811 CCCTGCTCCCGCAGCCCGCCCATCCAGTGGGGATTAAGTAAAGGGTCAAGGGAGAGCA 1870
Db 4639 CCCTGCTCCCGCAGCCCGCCCATCCAGTGGGGATTAAGTAAAGGGTCAAGGGAGAGCA 4698
QY 1871 GTCTGCTCTCTGT 1930
Db 4699 GTCTGCTCTCTGT 4758
QY 1931 AGCCCTGAGAGATTCCTGT 1990
Db 4759 AGCCCTGAGAGATTCCTGT 4818
QY 1991 CTTTGTGGAGT 2050
Db 4819 CTTTGTGGAGT 4878
QY 2051 CTTGCTCAGCATTCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2110
Db 4879 CTTGCTCAGCATTCCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4938
QY 2111 TTGGGAGGCTTGGCCCTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2170
Db 4939 TTGGGAGGCTTGGCCCTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4998
QY 2171 CTTGCAATGAAGT 2230
Db 4999 CTTGCAATGAAGT 5058
QY 2231 GTATAGAGAGTCAAAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2290
Db 5059 GTATAGAGAGTCAAAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5118

QY 2291 GGATACCTGCTCACTAGCTGTGAGAGTCTCTGAGAGTGAAGAGATGATGAGAGGAGGAGAG 2350
 DB 5119 GGATACCTGCTCACTAGCTGTGAGAGTCTCTGAGAGTGAAGAGATGATGAGAGGAGAGAG 5178
 QY 2351 AGCTTCATTTTGTGCTCTCTGAGAGCCTGTTATTTGTTGTTATTTCTGCTTCTTCCAG 2410
 DB 5179 AGCTTCATTTTGTGCTCTCTGAGAGCCTGTTATTTGTTGTTATTTCTGCTTCTTCCAG 5238
 QY 2411 TCCTGAGTGGAGTGGCTGCTGTAACCTGAACTCATGAGCCTTAAGAGAAAGAGAGAAACA 2470
 DB 5239 TCCTGAGTGGAGTGGCTGCTGTAACCTGAACTCATGAGCCTTAAGAGAAAGAGAGAAACA 5298
 QY 2471 ATTAGAGCTGGCAATGAGAGCTGGAGGAGAGAGTACAGCCAGCCAGAGTGTCCA 2530
 DB 5299 ATTAGAGCTGGCAATGAGAGCTGGAGGAGAGAGTACAGCCAGAGTGTCCA 5358
 QY 2531 GCCTTACCTGGGTCTTACCTGTGGCCAAACAGAGAGGAGTGTATACCTCTTCTTCTCT 2590
 DB 5359 GCCTTATGAGGTCTTACCAATGGGCCAAACAGAGGAGTGTATACCTCTTCTTCTCTCT 5418
 QY 2591 AGATGCCCACTCTCAATCTCAAGCCCAAGTCTCTCCACCTTACGAGGAGGCTGTGC 2650
 DB 5419 AGATGCCCACTCTCAATCTCAAGCCCAAGTCTCTCCACCTTACGAGGAGGCTGTGC 5477
 QY 2651 ATGGCAATACCTCATATCTGATTTGAGAGTTGACCTTTACAGAGGAGAGATTTTCTGCT 2710
 DB 5478 ATGGCAATACCTCATATCTGATTTGAGAGTTGACCTTTACAGAGGAGAGATTTTCTGCT 5537
 QY 2711 CAGTTCAACATGAATGAAGAGAACTCCTCTTTCTACAGCTCACTTATACAGAGGC 2770
 DB 5538 CAGTTCAACATGAATGAAGAGAACTCCTCTTTCTACAGCTCACTTATACAGAGGC 5597
 QY 2771 CCAGGTGCTCAGAGCCATGAGTGTCTTTTCTGGAGTGAAGAGTGAAGTAACT 2830
 DB 5598 CCAGGTGCTCAGAGCCATGAGTGTCTTTTCTGGAGTGAAGAGTGAAGTAACT 5657
 QY 2831 CCCAGTTCTGAGAGGAGTCTCTGAGAGTGTCTTGTGAGACCCCTACAGAGCCCTG 2890
 DB 5658 CCCAGTTCTGAGAGGAGTCTCTGAGAGTGTCTTGTGAGACCCCTACAGAGCCCTG 5717
 QY 2891 GATAGGACAGCCATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
 DB 5718 GATAGGACAGCCATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5777
 QY 2951 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010
 DB 5778 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5837
 QY 3011 CTGAACCTGGCAATTAACATCACTCTGCAAGCC 3045
 DB 5838 CTGAACCTGGCAATTAACATCACTCTGCAAGCC 5872

EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 896
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049, 020
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 876
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 895
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 884
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 894
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 971
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 964
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 882
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 899
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 893
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 900
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 901
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 892
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 915
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049, 019
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 970
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 972
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 916
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049, 373
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 875
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/049, 374
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 917
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 949
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 974
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 883
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 962
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 963
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 877
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/048, 878
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/070, 923
 EARLIER FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 60/092, 921
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/094, 657
 EARLIER FILING DATE: 1998-07-30
 NUMBER OF SEQ ID NOS: 1227
 SOFTWARE: PatentIn Ver. 2.0

RESULT 7
 US-09-205-258-74
 / Sequence 74, Application US/09205258
 / Patent No. 6525174
 / GENERAL INFORMATION:
 / APPLICANT: Young et al.
 / TITLE OF INVENTION: 207 Human Secreted Proteins
 / FILE REFERENCE: P2007P1
 / CURRENT APPLICATION NUMBER: US/09/205, 258
 / EARLIER FILING DATE: 1998-12-04
 / EARLIER APPLICATION NUMBER: PCT/US98/11422
 / EARLIER FILING DATE: 1998-06-04
 / EARLIER APPLICATION NUMBER: 60/048, 885
 / EARLIER FILING DATE: 1997-06-06
 / EARLIER APPLICATION NUMBER: 60/049, 375
 / EARLIER FILING DATE: 1997-06-06
 / EARLIER APPLICATION NUMBER: 60/048, 881
 / EARLIER FILING DATE: 1997-06-06
 / EARLIER APPLICATION NUMBER: 60/048, 880

RESULT 9

US-09-016-434-1454
Sequence 1454, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1454:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9790789
US-09-016-434-1454

Query Match 8.5%; Score 265.8; DB 4; Length 1480;
Best Local Similarity 54.7%; Pred. No. 7, 1e-51;
Matches 611; Conservative 0; Mismatches 471; Indels 35; Gaps 3;

QY 100 CCGGTCCTCGAGAGCGATTCTGCGCCGCGCTCCCGGAGCCCTCGGCGCCCGCTAGAGCC 159
DB 30 CCCAGGCGAGCGAGCGGCTGAGGACCGCGCCCAAGCTCGGGCGCAACACGCGGGGCTC 89
QY 160 GCGATCACTTCTCCCTGTGACCAACCGGCGCTGACAGGTTAAGAGCTTGCAATGCCGTTT 219
DB 90 CCGAGCAGCCCGCCNNNGAGCCCGAGANCCCTGGCTGTGTCGGGGGCGCACTGGGCGCAT 149
QY 220 GGGTGTGCTGCTGAGGCGAAGAGAACTAATCAAGCCATCGAGGTGACTAGACA 279
DB 150 GCTGGGGGCGAGTGAAGCCCGAG-----GTGAGACAGCGCGAGCAATTGAGACATC 204
QY 280 TATGATTTGGAGCAGGTCACTCAAGACTGAGAGATTGTTGAAATCTTCCGGGCGAAGAC 339
DB 205 TAGGACTTCGGAATGTTCGGGCGAGGGGCGCTTTCGGAAGTATCTTGCGACAGAAAT 264
QY 340 AAGAGCAGGAGGCTGACACCTCAAGAAATTCAGAGAGGCGGCGCGCAAGGTG 399
DB 265 AAGAGAGCGAAGCTGGTGGCCATCAATGATTCAGAGAGGCGCTGAGAGGCGAAG 324

QY 400 CGGAAGCTGCCAAGACGAGATAGGATCTCAAGATGTGAGAGATCCCAATCCCTA 459
DB 325 GAAGGCGCATGGAGATAGATATGTGCTGTCTGACACAGATCAAGCACTCCCAATTTGTA 384
QY 460 CAGCTGTGAGATGTGTTTGTGACCCGCAAGAGTACTTATCTTCTGAGCTGGCCAGC 519
DB 385 GCCCTGGATGACATCATATAGATGTGGGGCGACCTTACTCTCATATGAGCTGGGTGTG 444
QY 520 GGAAGGAGAGTGTGATCTGATCTGACACAGGCTTACTTCCGAGGAGACACAC 579
DB 445 GTGGGAGAGCTTTTGAACCGTATTTGGAAAAAGGCTTCTACACGAGGCGGACCGCAC 504
QY 580 AAGTGTACGCGAAGTCTGAGAGCGCGGCTATTGCACTCACTCAAGATCGGCGAC 639
DB 505 CGCTCATCTTCAGGTGTGATGTGTAATATCTCATATGACTGGGCAATTGTAC 564
QY 640 AGGATCTCAAGCTGAGAGACCTGTTTACTACAAACCGGCTGAGAACTGAAATTTGTC 699
DB 565 CGGATCTCAAGCCAGAGATCTGCTGTACTACAGCTGAGTGAAGATCCCAAAATCATG 624
QY 700 ATCACTGACTTCCATCTGCTAAGCTAAGAAA-----TGGCTCATCAAGAGCCCTGT 753
DB 625 ATCTCGAATTTGGCTCTCCAGATGAGAGACCCGGGCAAGTGTGCTTCCACCGGCTGT 684
QY 754 GGAACCCCGAGTATCTGCCCCGAGAGGTGTAGGCGGCGAGCGGTATGAGAGCCCTGT 813
DB 685 GGAATCTCCGAGATACGTGCGCCCTGAAGTCTGGCCCAAGGCTTACAGCAAGGCTGTG 744
QY 814 GACTGCTGGGCGCATGAGATCATATGATCATCTGCTTCAAGGCAATGCATCTTCTAT 873
DB 745 GATTGCTGTGTCATAGATGTCTATGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCT 804
QY 874 GAGAGGTGAGAGAGATGATTATGAGAACATGATAGAAATCTTCCGAGATCTG 933
DB 805 GAGGAG-----AATGAGCCAACTCTTTGAACAGATTTTG 840
QY 934 GCTGTGACTATGATTTGATCTCTCATATGAGATGATTTTGGAGGCGAGCGCAAGAC 993
DB 841 AAGGCGAGTACAGATTTGATCTCTCTTACTGGGAGCAATCTGATCTGCGCAAGAT 900
QY 994 CTGTGCAAGGCTGATGAGGTGAGAGCAAGACCAAGGATCATCTGCAAGAGGCGCAT 1053
DB 901 TTATTCGGGCACTGTATGAGAGAGCCAGAGAAAGATTCCTGTGAGCGGCTTG 960
QY 1054 TCCATGATGATTTCTGCAATGCTGCTTGTATAGAACTCAAGATGATGATCTG 1113
DB 961 CAGCACTCATGATTTGAGAGATACAGCTTATGATTAAGATTTCCACAGTGGTGAAT 1020
QY 1114 GCCCAGATTGAAAAAATTGCGCAGGGCCCAAGTGAAGAGGCTGTCCGATGACCAAC 1173
DB 1021 GAGAGATTCAGAGAACTTTGCGCAGAGCAAGTGAAGCAACCTTCAATGCGAGGCT 1080
QY 1174 CTATGAAGCGGCTCCGGGCAACAGAGCACTCCAGCA 1210
DB 1081 GTGGTGGCGCATGAGGAATTCGACGTGGGACCA 1117

RESULT 10

US-09-016-434-543
Sequence 543, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

Thu Apr 29 08:44:17 2004

us-10-669-689-1.rn1

Page 13

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COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
CLONE: 2342912
US-09-016-434-543
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Query Match 8.3%; Score 258; DB 4; Length 264;

Best Local Similarity 97.7%; Pred. No. 1,9e-49;

Matches 258; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 515 CCACGGGAGGAGGAGTGTTCATCGATCGATCGACGAGGCTACTCTCGAGGAGACA 574
DB 1 CCACNGAGGAGGAGTGTTCATCGATCGATCGACGAGGCTACTCTCGAGGAGACA 60
QY 575 CAACGAACTGTGATCGCAAGTCTGTGAGGCGGTCTATTGCTCACTCAAGATCG 634
DB 61 CAACGAACTGTGATCGCAAGTCTGTGAGGCGGTCTATTGCTCACTCAAGATCG 120
QY 635 TGCACAGGAATCTCAAGTGTGAGAACTGTGTTTCTACACCGGCTGAAGAACTCGAAGA 694
DB 121 TGCACAGGAATCTCAAGTGTGAGAACTGTGTTTCTACACCGGCTGAAGAACTCGAAGA 180
QY 695 TTGTCACTAGGATCTTCATCTGCTAAGTAAAGTGGCTCATCAAGGAGCCCTGTG 754
DB 181 TTGTCACTAGGATCTTCATCTGCTAAGTAAAGTGGCTCATCAAGGAGCCCTGTG 240
QY 755 GGACCCCGAGTATCTGGCCCGAG 778
DB 241 GGACCCCGAGTATCTGGCCCGAG 264
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RESULT 11

US-09-579-664B-3

Sequence 3, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Bird, Timothy A.

APPLICANT: Vireo, G. Duke

APPLICANT: Martin, Unja

APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REFERENCE: 2923-A

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 36

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SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1694
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-579-664B-3
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Query Match 8.0%; Score 249.2; DB 4; Length 1694;

Best Local Similarity 55.7%; Pred. No. 4.4e-47;

Matches 538; Conservative 0; Mismatches 398; Indels 30; Gaps 2;

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QY 251 ATAACGAGCATCGAGGAGCTGACATATATGATTTGGACAGGCTCAAGACTGAGG 310
DB 280 AAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 339
QY 311 AGTTTGTGAATCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 370
DB 340 CTTTCTGAGATTTGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
QY 371 AGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 430
DB 400 GCATCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459
QY 431 TGAAGATGTGAAGATCCCAATCTCAAGCTGTGATGTGATGTGATGTGATGTGATGTG 490
DB 460 TTGAAGATGTGAAGATCCCAATCTCAAGCTGTGATGTGATGTGATGTGATGTGATGTG 519
QY 491 AGTACTTATCTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
DB 520 ACCCTTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 579
QY 551 AGGCTACTACTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 610
DB 580 AGGCTACTACTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 639
QY 611 CTTTATTTGATCTCACTCAAGATGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 670
DB 640 ACTTATCTCAAGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
QY 671 ACAACCGGTGAAGATCTCAAGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 727
DB 700 ACAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 759
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QY 785 TAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 844
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QY 845 TCTGTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 904
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DB 916 ATGATTAAGATCTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
QY 965 GGGATGATTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1024
DB 976 GGGATGATTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1035
QY 1025 ACCAGCGATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1084
DB 1036 ATTAAGATTAAGATTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1095
QY 1085 CTGATTAAGATCAAGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 1144
DB 1096 TTAGCAAAACATCAAGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 1155
QY 1145 AGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1204
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Db 1156 AATGAGACAGGTTTAACGCCACGCGACGTGCTGAGACATATGCGGAGGCTCCAGCTTG 1215
QY 1205 CCAGCA 1210
Db 1216 GCAGCA 1221

RESULT 12
US-09-230-896C-5
; Sequence 5, Application US/09230896C
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Sutcliffe, et al.
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
; FILE REFERENCE: TSRI-548.1
; CURRENT APPLICATION NUMBER: US/09/230,896C
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/023,220
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: ratus ratus
US-09-230-896C-5

Query Match 8.0%; Score 249; DB 4; Length 1458;
Best Local Similarity 55.7%; Pred. No. 4.5e-47;
Matches 539; Conservative 0; Mismatches 405; Indels 27; Gaps 2;
QY 249 CTATTAACGACCATCGAGGTGA CTGACGATGATGTTGGGACAGGTCATCAAGCTGA 308
Db 61 CAAAGAAACAGACGAGGACATCAAGTGTCTATGAGATCCGGAGAAAGCTGGGCTCGGG 120
QY 309 GGAGTTTGTGAATCTTCCGGCCCAAGACAGACAGCAGCAGCTGACACCTGCAA 368
Db 121 TGGCTTCTCGAGGTATGTGTGCCAGAGAAAGGGCTCTGCTCACTTGTGGCCCTCA 180
QY 369 GAAGTTCAGAACGGGACGGCGCAAGGTGCGGAAAGCTGCCAAGACGAGATGAGCAT 428
Db 181 GTGCATGCCAAGAAAGCACTTGGGCAAGAGCCCTGTGTGAGAAATGAGATCGAGT 240
QY 429 CTTCAAGATGTGAAGATCCCAACATCTTACAGCTGTGTGAGATGTTGTGACCCGCAA 488
Db 241 ACTCCGAGAGATTAGCCACCACCAATGTGCTCTGAGAGAGTCCACAGAGGCGCTTC 300
QY 489 GGAATCTTATCTTCTGTGAGCTGGCCACAGGGAGGAGTGTGACCTGATCTGGA 548
Db 301 CCACTTCTACTTGGCCATGAGCTGTGTACAGGTGTGTAACCTTTGACGAAATCATGA 360
QY 549 CCAAGGCTACTACTCGAGCGAGACACAAACAACTGTGTACCGCAAGCTCTGAGGCGCT 608
Db 361 GCGGGGCTCTTACACAGAGAGATGAGACCACTTGTAGGGCAGAGTCTGTGTGTCTGT 420
QY 609 GGGCTTATTTGCACTCAAGATCGTGACAGAGAACTTCAAGCTGAGAACTGTGTTTA 668
Db 421 CTCCTACCTTCATAGCCTGGGCACTCGTGACCGGACCTTCAACCTGAAAACTCTCTTA 480
QY 669 CTTCACACGGGCTGAAGACTCGAAGATGTTCATCAGTACGATTCATCTGGCTAAGTAA 728
Db 481 TGCACACCTTTTGAGGACTCCAAAGATCATGTCTGTGATTTGGCTGTCCAAAAATTA 540
QY 729 AAATGAGCTCATCAAGA---GCCCTGTGGGACCCCGAGATATCTGGCCCAAGGTGCT 785
Db 541 AGCTGGCAACATGTGTAGGCAAGCTGTGGGACCCAGATATGTGGCCCAAGCTCCT 600
QY 786 AGGCGGACGCGTATGAGACGCGCTGTGA CTGCTGGGCGCATTTGAGTCACTCATGTACT 845
Db 601 GGAGCAAAACCCCTACGGAAGGCGGTAGATGTGTGGCCCTGGGTGTACTTCTACAT 660
QY 846 CTGTCTTTCAGGCAATCACTTTCTATGTAGAGGTGGAAGAAATGATTTATGAGACCA 905

Db 661 CTTCTGTGTGGTACCCCTTTCTATGATGAGAGGATCCCTGAA----- 706
QY 906 TGATTAAGATCTCTTCCGAGAGATCTGTGCTGTGATGATGATTTGACTTCCATATTG 965
Db 707 -----CTCTTACGACAGATTTCTGAGGCGACGATGACGATTTGACTCTCCCTTTTG 756
QY 966 GGATGATATTTCCGAGGACGACCAAGACTGTGTCAAGGCTGATGAGGTGAGACAGA 1025
Db 757 GGATGACATCTCAAGATCCAGCAAGACCTTCAATTCGGACCTTCTGGAAGGTATCCCA 816
QY 1026 CCAAGGATCATCTGCAAGAGGACATCTCCATGATGATTTCTGGCAATGCTGCTTC 1085
Db 817 GAAAGGTTCCTCGCCAAAGGCTTTACAGCATCTTGGATCTTGGGATGACGCTT 876
QY 1086 TGATTAAGATCTCAAGATGATGTGTGTGCTGCTGAGATGAAAGAACTTTGCCAGGCCAA 1145
Db 877 GGACAGGACATCTTAAAGTCTGTCACTGAGCAGATCCAGAAATTTTCCAGGACCA 936
QY 1146 GTGAGAGAGGCTGTCCGAGTACCACTCTCATGAAAGCGCTCCGGGACCAAGCAGTC 1205
Db 937 CTGGAAGGTCATTCATGACCATCATTCCTACGTCACATCCGTAACTGGGACAGAG 996
QY 1206 CAGCAGGCTG 1216
Db 997 CCCAGAGGTG 1007

RESULT 13
US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wenman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundang
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillingshaast
; APPLICANT: Drmanac, Radole T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1372)
US-09-620-312D-526
Query Match 7.8%; Score 244.8; DB 4; Length 1733;
Best Local Similarity 53.7%; Pred. No. 4.5e-46;
Matches 597; Conservative 0; Mismatches 482; Indels 33; Gaps 3;

QY 108 CGAGGCGAATTCGCCCCCGGCGGAGCCCTCGGCGCCCGCTGAGCCCGCATCAC 167
DB 106 CGAGGCGGAGCGGCGGCGGCGCATCCCGCGCGCTCTGCGCCCGGCGCGCGCCCGCGCGCG 165
QY 168 TTCTCTCTCTGACCAACCGGCGCTGCGAGTTGAGCTTGGCAATGCCGTTTGGGTGTGT 227
DB 166 CCGTCCCGACCGCGCGCGCGCGCTCTCGGCGCGCGCTCTCGCGCATGCGCGCGCG 225
QY 228 GACTCTGGGCGGACAGAAAGTAATTAACAGCATGCGGAGG---TGACTGACGATATGA 284
DB 226 GAACGCGGAGAGCGCTCTCTCGGAAAGCAAGCTGAAGACATCAAGAGATCTTCA 285
QY 285 TTGGGACAGGTCATCAAGACTGAGAGTTTGGTAATCTTCGCGGCGCAAGACAAGAC 344
DB 286 GTTCAAGAGACCTCGGAGCGGCGCGCTTTCCGAGTGGTTTACCTGAGAGAGAGCG 345
QY 345 GACAGCGGAGCTGCACTGCAAGATTTCAGAAAGCGGAGCGCGCAAGGTGCGGAA 404
DB 346 AACTGGCAAGCTTTGTCTGTGAAGTATCTCTAAGAGAGCGGTGAAGGCGCAAGGAAAG 405
QY 405 AGCTGCCAAGACAGATAGGCACTCTCAAGATGCTGAAGCATCCCAATCTCAAGCT 464
DB 406 CAGCATGAGAAATGATAGCGCGCTCTGAGAAAGATTACATGAAATAATGTGCGCT 465
QY 465 GGTGGAATGTGTGTGACCCGCGAAGAGTCTTATCTCTGAGAGTGGCCAGCGGAG 524
DB 466 GGAAGACATTTATGAAGCCCAATCACTGTACTTGTATGATGAGTGTGTCGCGTGG 525
QY 525 GGAAGTGTGTGACTGATCTCTGACCAAGGCTACTACTCGGAGCGAGACAAGACAAGT 584
DB 526 AGAGCTTTTGAACCGGATAGTGAAGAGGCTTTTATACAGAAAGATGCCAGCATCT 585
QY 585 GGTACGCGAAGTCTGAGGCGCGTGTGCTTATGCACTCACTCAAGATGTGACAGAA 644
DB 586 GATCCGCGAAGTCTGAGCGCGGTACTATCTCAAGATGGGCACTGTCCACAGAGA 645
QY 645 TCTCAAGCTGAGAACTGTTTACTACACCGGCTAAGAACTCGAAGTGTCTATCAG 704
DB 646 CCTCAAGCGCGAATCTCTGTACTACAGTCAAGATGAGAGAGTCCAAATTAATGATCAG 705
QY 705 TGACTTCATCTGCTAAGCTAG-----AAATGCGCTCATCAAGAGCGCGTGGGAG 758
DB 706 TGACTTTGATTTGCAAAATGAGGCGAAGAGATGTATGCTCACTGCTGTGAAAC 765
QY 759 CCGCGAGTATCGGCGCGCGAGAGTGTAGGCGGCGAGCGGATGAGCGCCCTGTGACTG 818
DB 766 TCCAGGCTATGTGGCTCTCTGAAATCTCGCCGAGAACTTACAGCAAAAGCGTGAAGT 825
QY 819 CTGGGCGCATTTGAGATCATGATCATCTCTGCTTTCAGGCAATCACTTTCTATGAGGA 878
DB 826 CTGCTCATCGAGATGATGCTGCTACATCTTGTCTGCGGCTACCTCTCTT----- 876
QY 879 GGTGAGAAAGATATATGAGAACCATGATTAAGAAATCTCTGCGCAAGTCTGCGTGG 938
DB 877 -----TTATGATGAAGATGATCTCAAGCTCTTTGAGCAGATCTCTCAAGGC 921
QY 939 TGACTATGATTTGATCTCTCATATTTGGGATGATTTTGGAGGCGAGCGCAAGAGCTGAT 998
DB 922 GGAATATGAGTTTATCTCTCTCTCTGAGATGATCTCTCGACCTTCCAAAGACTTTCAT 961
QY 999 CACAAGGCTGATGAGAGTGAAGCAAGACAGCGGATCACTGACAGAAAGGCGCATCTTCCA 1058
DB 982 TCGGAACCTGATGAGAGAGCCCGAATTAACGATGAGAGAGGAGTGTGCGCA 1041
QY 1059 TGAATGATTTCTGCAATGCTCTCTCTGATTAAGACATCAAGATGTGTGTGTGCGCA 1118
DB 1042 CCGATGATGCTGCTGTGACAGAGCGCTCAACAAAGACATCCACAGATGCTGCAAGCGCA 1101
QY 1119 GATTGAAAGAACTTTGCAAGGCGCAAGTGAAGAGGCTGTGCAAGTGAAGCAAGCTCAT 1178
DB 1102 GATCCGAGAAAGCTTTGCAAGAGCAAGTGAAGCAAGCATTTAATGCAAGGCGCGTGT 1161

QY 1179 GAACGCGCTCCGCGCACCAAGCAAGTCCAGCA 1210
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RESULT 14
US-08-989-12
Sequence 12, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Puri
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878, 989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-08-878-989-12
Query Match 7.8%; Score 242.6; DB 2; Length 1282;
Best Local Similarity 55.3%; Pred. No. 1.2e-45;
Matches 529; Conservative 0; Mismatches 400; Indels 27; Gaps 2;
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RESULT 15
US-09-272-796-12

Sequence 12, Application us/09272796

Patent No. 6207148

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl G.

APPLICANT: Goli, Surya K.

APPLICANT: Shah, Puri

TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

TITLE OF INVENTION: KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-09-272-796-12
Query Match 7.8%; Score 242.6; DB 3; Length 1282;
Best Local Similarity 55.3%; Pred. No. 1.2e-45;
Matches 529; Conservative 0; Mismatches 400; Indels 27; Gaps 2;
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FEATURES
source

Location/Qualifiers
1. .3124
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 3124; DB 6; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AX350342 GI:18616005
VERSION AX350342.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 Yan, C.C., Wei, M.H., Ketchum, K.C., Merkulov, G.C. and Beasley, E.M.
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human Kinase proteins, and uses thereof
Patent: WO 0192492-A 1 06-DEC-2001;
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location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 661 CTGCTTTAATAACACCGCTGAGAACTCGAAGATGTGATCACTGATCTTCCATCTGCT 720
DB 661 CTGCTTTAATAACACCGCTGAGAACTCGAAGATGTGATCACTGATCTTCCATCTGCT 720
QY 721 AAGCTAGAAATGAGCTTCATCAAGAGCTGTGTGAGACCCCGAGTATCTGCGCCAGAG 780
DB 721 AAGCTAGAAATGAGCTTCATCAAGAGCTGTGTGAGACCCCGAGTATCTGCGCCAGAG 780
QY 781 GTGTAGGCGCGGACGCGGTATGAGCGCCGTGTGACGTGTGCGCATTTGAGTGCATATG 840
DB 781 GTGTAGGCGCGGACGCGGTATGAGCGCCGTGTGACGTGTGCGCATTTGAGTGCATATG 840
QY 841 TACATCTGCTTTAGAGCAATCCACTTTCTATAGAGAGGTGAGAAAGATGATTATGAG 900
DB 841 TACATCTGCTTTAGAGCAATCCACTTTCTATAGAGAGGTGAGAAAGATGATTATGAG 900
QY 901 AACCATGATTAAGAACTCTTCCGCAAGATCTGTGCTGTGATGATGATTTGACTCTTCA 960
DB 901 AACCATGATTAAGAACTCTTCCGCAAGATCTGTGCTGTGATGATGATTTGACTCTTCA 960
QY 961 TATTGGATGATATTGTGCGAGGCGCCAAAGACTGTGTGATGATGATGATGATGATG 1020
DB 961 TATTGGATGATATTGTGCGAGGCGCCAAAGACTGTGTGATGATGATGATGATGATG 1020
QY 1021 CAAGACCAAGGATCACTGCGAAGAGGCGATCCCATGAGTGTGATTTGCGCAATGCT 1080
DB 1021 CAAGACCAAGGATCACTGCGAAGAGGCGATCTCCCATGAGTGTGATTTGCGCAATGCT 1080
QY 1081 GCTTCTGATTAAGAACTATCAAGATGTGTCTGTGCCAGATTGAAAGAACTTTGCCAGG 1140
DB 1081 GCTTCTGATTAAGAACTATCAAGATGTGTCTGTGCCAGATTGAAAGAACTTTGCCAGG 1140
QY 1141 GCCAAGTGAAGAGGCTGTCCAGTGAACAACCTCATGAAACGCTTCGCGGACACAGAG 1200
DB 1141 GCCAAGTGAAGAGGCTGTCCAGTGAACAACCTCATGAAACGCTTCGCGGACACAGAG 1200
QY 1201 CAGTCAACAGCGCTGCGACGCCCAATGCGCTTCAGCCACAGCAATTCGCCACCCCGGGCT 1260
DB 1201 CAGTCAACAGCGCTGCGACGCCCAATGCGCTTCAGCCACAGCAATTCGCCACCCCGGGCT 1260
QY 1261 GCAAGTGGGCGCAACGCTGAGCTGCGAGTGAAGTCACTCAGGCGCTGAGGATGATGCT 1320
DB 1261 GCAAGTGGGCGCAACGCTGAGCTGCGAGTGAAGTCACTCAGGCGCTGAGGATGATGCT 1320
QY 1321 GCTGTGTGCAAGAGTATGATGTGAGCCCGCAAGCGTGTGCTCAACCCAGCCCA 1380
DB 1321 GCTGTGTGCAAGAGTATGATGTGAGCCCGCAAGCGTGTGCTCAACCCAGCCCA 1380
QY 1381 GATGGAAGTGCACCCCACTGATGAGGAGTGTCAACCCAGCCCAAGGATGAGGATC 1440
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[illegible]

Db	2521	CAGGTGTCACGCCCTTACTGGAGTCCTTAACCCTGGGCCAAACGGAAGGCGTAGTAACCTCCT	2580
Oy	2581	TGCCTCTTCCATAGATGCCCCACCTCCTCAACAATCTGAGGCCAACAGTCTCTCACCTTAGAGG	2640
Db	2581	TGGCTCTTGCTAGATAGGCCACCTCCTACAAATCTCAGGCCCAAGAAGCTCTCCACCTTAGGG	2640
Oy	2641	GCGCTGCTGCATGCGCAATAACTCATATCTGATATTGAGGTTGGCCCTTTACAGGGGACG	2700
Db	2641	GCGCTGCTGCATGCGCAATAACTCATATCTGATATTGAGGTTGGCCCTTTACAGGGGACG	2700
Oy	2701	ATTTCCTGCTCAGTGTCAAATGAATGAAGAGAATCCCTCCTTTCTACAGCTCACTTC	2760
Db	2701	ATTTCCTGCTCAGTGTCAAATGAATGAAGAGAATCCCTCCTTTCTACAGCTCACTTC	2760
Oy	2761	TATCAGAGGCCCAAGTGGCTCAAGACCAATGATGTGCTTTTCTTGGAGTAGAGAGTA	2820
Db	2761	TATCAGAGGCCCAAGTGGCTCAAGACCAATGATGTGCTTTTCTTGGAGTAGAGAGTA	2820
Oy	2821	GCGTTAAATCTCCCAGATTTCTGTGAGGAGGCTCTGCAAGATGCCCCCTTTGTCAACCCTA	2880
Db	2821	GCGTTAAATCTCCCAGATTTCTGTGAGGAGGCTCTGCAAGATGCCCCCTTTGTCAACCCTA	2880
Oy	2881	CCAAGAGCTGGATAGGAGAGCAATTTGTCCTGGCCCTTGCTGGGCACTCCGATGTGCTC	2940
Db	2881	CCAAGAGCTGGATAGGAGAGCAATTTGTCCTGGCCCTTGCTGGGCACTCCGATGTGCTC	2940
Oy	2941	CTGCCCCCTTCCCTCGCATGCTGCTGTGGTCTGCTCTGTGTGTGAGAGTTCGATGGGTTAC	3000
Db	2941	CTGCCCCCTTCCCTCGCATGCTGCTGTGGTCTGCTCTGTGTGTGAGAGTTCGATGGGTTAC	3000
Oy	3001	TGTGTGCTCTA CTGAACTGGCGAAATTAACATCACTCCGCAAGCCCAAAAAAAAAAAAAA	3060
Db	3001	TGTGTGCTCTA CTGAACTGGCGAAATTAACATCACTCCGCAAGCCCAAAAAAAAAAAAAA	3060
Oy	3061	AAA	3120
Db	3061	AAA	3120
Oy	3121	AAAA 3124	
Db	3121	AAAA 3124	
RESULT 4	BC019256	3057 bp	mRNA linear PRI 03-OCT-2003
LOCUS	BC019256		
DEFINITION	Homo sapiens hypothetical protein MGC8407, mRNA (cDNA clone		
ACCESSION	BC019256		
VERSION	BC019256.1		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eumalia; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 3057)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,		
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmer,C.M., Schuler,G.D.,		
	Altschul,S.F., Zeeberg,B., Buelow,K.H., Schaefer,C.F., Bhat,N.K.,		
	Hopkins,R.F., Jordan,H., Moore,T., Wax,S.I., Wang,J., Heien,F.,		
	Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.W., Hong,L.,		
	Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,		
	Scheetz,T.E., Brownstein,M.J., Uddin,T.B., Toshiyuki,S.,		
	Carninci,P., Prange,C., Raha,S., Locoellano,N.A., Peters,G.J.,		
	Abramson,R.D., Mulianhy,S.J., Boesek,S.A., McEwen,P.J.,		
	McNernan,K.U., Malek,U.A., Gunaratne,P.H., Richards,S.,		
	Woley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huily,S.W.,		
	Vallalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,		
	Fahney,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,		
	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,		
	Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,		
	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,U., Myers,R.M.,		

QY	1148	GGAGAAGGCTGTCGAGTGAACCACTCTGATGAAAAGGCTCCGGGCAACAGAGCTGCA	1207
DB	1081	GGAGAAGGCTGTCGAGTGAACCACTCTGATGAAAAGGCTCCGGGCAACAGAGCTGCA	1140
QY	1208	GCACGGCTGACAGCCAGTGGCTCAGCCACAGACACTGSCACCCCGGGCTGACAGT	1267
DB	1141	GCACGGCTGACAGCCAGTGGCTCAGCCACAGACACTGSCACCCCGGGCTGACAGT	1200
QY	1268	GGGCCACAGCTGACGCTGAGTGAAGTACTCAGACCCCTGAGGGTGAATGCTGCTGTG	1327
DB	1201	GGGCCACAGCTGACGCTGAGTGAAGTACTCAGACCCCTGAGGGTGAATGCTGCTGTG	1260
QY	1328	CTGCAAAAGTGAATATGTGGCCCCCGGAGAACCTTAATGTCACCCCAAGCACAATGGA	1387
DB	1261	CTGCAAAAGTGAATATGTGGCCCCCGGAGAACCTTAATGTCACCCCAAGCACAATGGA	1320
QY	1388	GTGCCACCCCAAGCACACTGATGGAGTGTACCCCAAGCACAAGATGAAATCACTCCAG	1447
DB	1321	GTGCCACCCCAAGCACACTGATGGAGTGTACCCCAAGCACAAGATGAAATCACTCCAG	1380
QY	1448	CCACTGATGGAGTGTACCCCAAGTGTACAGAGAGCGCTACTCCAGCACTGATGGA	1507
DB	1381	CCACTGATGGAGTGTACCCCAAGTGTACAGAGAGCGCTACTCCAGCACTGATGGA	1440
QY	1508	GAGCCACACAGCACAAGAAAGAGCACTGTGCCCAACCCCAAGCACTGCTGTG	1567
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DB	1501	CCACCAAGGAGTGTGCAACCCCTGAGCCGAGCTATGGCCCAAGCCGAGCACAAGCCCA	1560
QY	1628	AGGGCCCAAGGAGGAGGCTCAACCTCTAATGAAAGGAGAGGCTGTGTTATGCC	1687
DB	1561	AGGGCCCAAGGAGGAGGCTCAACCTCTAATGAAAGGAGAGGCTGTGTTATGCC	1620
QY	1688	AGGAGTCTCAAAAGGAGAGGAGGAGCTGATGAGGAGCGCTGTGAGGGGGAGGAGAT	1747
DB	1621	AGGAGTCTCAAAAGGAGAGGAGGAGCTGATGAGGAGCGCTGTGAGGGGGAGGAGAT	1680
QY	1748	GGGAGAGAGGAGTGGAGAGTGAATGAAGGGCTTCTCACTGTATATGATCACTGGCATG	1807
DB	1681	GGGAGAGAGGAGTGGAGAGTGAATGAAGGGCTTCTCACTGTATATGATCACTGGCATG	1740
QY	1808	ATGCCCTGCTCCCAATGCCCCCAATCCAGTGGGGCAATACTGAGGGGTACCGGAGA	1867
DB	1741	ATGCCCTGCTCCCAATGCCCCCAATCCAGTGGGGCAATACTGAGGGGTACCGGAGA	1800
QY	1868	GCAGTCTGCTCTCTGTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT	1927
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QY	1928	CCCAAGCCCTGATGATGATCTCTGTGTGTCTTCTGCTCTTGTGTAAGTCTTCAAGTTCT	1987
DB	1861	CCCAAGCCCTGATGATGATCTCTGTGTGTCTTCTGCTCTTGTGTAAGTCTTCAAGTTCT	1920
QY	1988	GTTCTTGTGGAGTGTGCTCTGAGGATACTCAAGGGGGCTCCGCTCTGCTCCCTTCC	2047
DB	1921	GTTCTTGTGGAGTGTGCTCTGAGGATACTCAAGGGGGCTCCGCTCTGCTCCCTTCC	1980
QY	2048	CTTCTTGTCTCACCAATCCCTGAGGAGGAGGCTGAGAGTCCACACTCTCCAGGCTCTA	2107
DB	1981	CTTCTTGTCTCACCAATCCCTGAGGAGGAGGCTGAGAGTCCACACTCTCCAGGCTCTA	2040
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DB	2041	AACTTGGGCGGCTTGTGCTGAGAGTGTCTTCCAGCGAGGCTCTGACGGCTCTTAG	2100
QY	2168	GCTCTTGTCAATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2227
DB	2101	GCTCTTGTCAATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2160
QY	2228	CTGGTATAGAGATGAGAAAGGTAGGGCAATGTTTAAATGTCAGACTTGGACATGGC	2287
DB	2161	CTGGTATAGAGATGAGAAAGGTAGGGCAATGTTTAAATGTCAGACTTGGACATGGC	2220
QY	2288	TAGGGATACTGCTCACTAGCTGTGAGGCTCTCAGAGTGTGAGAGAAATGATAGAGGCT	2347
DB	2221	TAGGGATACTGCTCACTAGCTGTGAGGCTCTCAGAGTGTGAGAGAAATGATAGAGGCT	2280
QY	2348	AGAACTTCAATTTTGTCTTCTTAAGACCTGTAATTTGTATTTTCTGCTTCC	2407
DB	2281	AGAACTTCAATTTTGTCTTCTTAAGACCTGTAATTTGTATTTTCTGCTTCC	2340
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DB	2341	GAGTCTGAGTGGGCTGCTGCTGACCTTAAGCTCATGAGCTCTTAAGGAAAGAGAG	2400
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DB	2401	ACAATTAGAGCGTGGCAATGAGACTTGGCAGGGCAAGTGAAGCCCAAGCACTCACTGTC	2460
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DB	2461	CCAGCTTACTGGGCTTACCTTGGCCAAACAGGAGGGCTGATACCTCTTGTCTT	2520
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DB	2581	TGCATGGCAATTAATCTCAATCTGATTTGGAGGTTTCCCTTTTACAGGGCAGATTTCT	2640
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DB	2641	GCTCAGTTCAACAAATGAATGAAGAGAACTCCCTCTTTTACAGCTCACTTCTATAGA	2700
QY	2768	GGCCCAAGGCTCTCAGAGCCACATGATGCTTTTCTGAGGAGTGGAGTTAA	2827
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QY	2828	ACTCCCAAGTTCTCTGAGGAGGCTCTGACAGTGCCTTTTGTACAGACCTTACACAGC	2887
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DB	2821	CTGGATAGGAGCCACATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2880
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QY	3008	CTACTGAACCTGGGAAATPAAATCAATCCCTGCAAGCCAAAGCAAAAAAAAAAAAAAA	3067
DB	2941	CTACTGAACCTGGGAAATPAAATCAATCCCTGCAAGCCAAAGCAAAAAAAAAAAAAAA	3000
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DB	3001	AA	3050
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BD127328			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
1 (bases 1 to 3022)			

AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2759 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2759
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC

COMMENT

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (194)..(1896).

FEATURES

source 1..3022
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 96.6%; Score 3018.8; DB 6; Length 3022;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3020; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
18 GTGGGAATCCGGTGCAGCGAGCTGGAGATCTGGAGTTCCGTACCGAAGCGGCT 77
1 GTGCGAATCCGGTGCAGCGAGCTGGAGATCTGGAGTTCCGTACCGAAGCGGCT 60
78 GCATCTGGCGCGCGTGTGCGCGCGCTGCGAGAGGAGATTCTGCCCGCGTCCCGGAG 137
61 GCATCTGGCGCGCGTGTGCGCGCGCTGCGAGAGGAGATTCTGCCCGCGTCCCGGAG 120
138 CCCCTGGCGCGCGCTGAGCGCGGATCATCTTCCCTGTGACCAACGCGCGCTGAG 197
121 CCTCTGGCGCGCGCTGAGCGCGGATCATCTTCCCTGTGACCAACGCGCGCTGAG 180
198 TTAGAGCTGGCAATGCGTTTGCGTGTGACTCTTGGCGAGCAAGAGAGATTAACA 257
181 TTAGAGCTGGCAATGCGTTTGCGTGTGACTCTTGGCGAGCAAGAGAGATTAACA 240
258 GCCATCGAGGTGACTGACAGATTTGATTGGAGCAGGTATCAAGCTGAGAGTTTGG 317
241 GCCATCGAGGTGACTGACAGATTTGATTGGAGCAGGTATCAAGCTGAGAGTTTGG 300
318 TGAATCTTCGGCGCGCAAGAGCAAGAGAGAGCTGACACCTGCAAGAGAGTTTCA 377
301 TGAATCTTCGGCGCGCAAGAGCAAGAGAGAGCTGACACCTGCAAGAGAGTTTCA 360
378 GAAGCGGAGCGCGCGAGAGTGGAGAGTGGCAAGAGAGAGAGATCTCTCAAGAT 437
361 GAAGCGGAGCGCGCGAGAGTGGAGAGTGGCAAGAGAGAGAGATCTCTCAAGAT 420
421 GGTAAGCATTCCTCAATCTTACAGCTGTGTGATTTGTGACCGCGCAAGAGATCTT 480
498 TATTTCTTGGAGCTGGCGCAAGAGAGAGAGTGTGATCTGAGATCTTGAACAGAGGCTA 557
481 TATTTCTTGGAGCTGGCGCAAGAGAGAGAGTGTGATCTGAGATCTTGAACAGAGGCTA 540
558 CTACTCGAGAGAGACCAAGCAACGTGTGACAGGCAAGCTCTGAGAGCGCTGAGCTATT 617
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QY 618 GCATCTCAAGATCGTGCAAGAGATCTCAAGCTGAGAACCTGGTTTACTACCAACCG 677
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QY 678 GCTGAAGACTGGAAGATTGATCATGAGATTTCCATCTGGCTTAAGTGAAGAAATGGCT 737
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QY 738 CATCAAGAGCGCTGTGGAGCCCCAGATCTGGCCCCAGAGGTGTAAGCGCGAGCG 797
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DB 1021 TGCAGAAAGGCGCATCTTCCATGATGATTTCTGCAATGCTCTTCTGATTAAGACAT 1080
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QY 1218 AGCCAGTCTGCGCTGAGCAAGACACTGCGCACCCCGCGGCTGAGTGGGCGCACAGC 1277
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QY 1278 TGCAGCTGAGTGAAGTACTAGCCCTGAGGGTGTGCTGCTGCTGCTGCAAGAG 1337
DB 1261 TGCAGCTGAGTGAAGTACTAGCCCTGAGGGTGTGCTGCTGCTGCTGCAAGAG 1320
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DB 1321 TGAATATGTGCCCCCGGAGACCGTATGTCACCCCAAGTGAAGTATGCAACCC 1380
QY 1398 AGCCATGATGCGAGTGTCAACCCAGCCAGATGGAAGCATCTCCAGGCACTGATG 1457
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Db 1691 AAGGAGAGAGCCAGCTAGTAGGCAAGCTGCTGAGAGGGGGGAGGGGATGGGAGAGG 1740
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 Homo sapiens CDNA FLJ90375.f1s, clone NT2RP2004670, highly similar
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 ACCESSION
 AK074856
 VERSION
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 KEYWORDS
 oligo capsding; file (full insert sequence).
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
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 Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
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 Kawai-Hio,Y., Saito,K., Yamamoto,J., Makamatsu,A., Nakamura,Y.,
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 Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
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 NEDO human cDNA sequencing project
 UNPUBLISHED
 2 (bases 1 to 3022)
 Isogai,T. and Otsuki,T.
 Direct Submission
 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kibetaru, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo; Laboratory of
 Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
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REMARK
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 On Aug 19, 2003 this sequence version replaced gi:12635450.
 COMMENT
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:12635450.
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
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 Young, A., Zhang, J., H. and Green, B.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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Best Local Similarity 99.9%; Pred. No. 0;
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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1623 CCCAAGAGCGGCCACAGGCAAGGCTTCAACCTCTATGAAAGGGAAGAGGCTGTGTTA 1682
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1743 GGAATGGGAGAGAGGTGGGAGAGTGAAGTGAAGGAGGCTTCTCATCTGTATCATAGATCATG 1802
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Dp	1861	CCGCCCCCAGCCCTGCAATGGAATTCCTGTGAGCTTTTCTGCTTTTGTACCTTACACAG	1920
Qy	1983	TTTTGTTCCTCTGTGGGATGCTGCTTAAGGATACTCAAGGGAGCTCTGCTCTCTCC	2042
Dp	1921	TTTTGTGTTCTCTGTGGGATGCTGCTTAAGGATACTCAAGGGAGGCTCTGCTCTCTCC	1980
Qy	2043	CTTCCCTTCTTGGCTCAACATTCCCCTAAGGAGGCTGACAGTCCCACTCTCCAG	2102
Dp	1981	CTTCCCTTCTTGGCTCAACATTCCCCTAAGGAGGCTGACAGTCCCACTCTCCAG	2040
Qy	2103	CCCTAACTTGGGGGGCTTGGCCCTGAGAGTGGTCCCTCAAGGAGGCTCTGAGGGT	2162
Dp	2041	CCCTAACTTGGGGGGCTTGGCCCTGAGAGTGGTCCCTCAAGGAGGCTCTGAGGGT	2100
Qy	2163	CTTAAAGCTCTGCACATGAGAGTGTGTGCTGTGGTGTGGGGCTGCTTAAGACAAAT	2222
Dp	2101	CTTAAAGCTCTGCACATGAGAGTGTGTGCTGTGGTGTGGGGCTGCTTAAGAGCAAT	2160
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Dp	2161	ACAGGCTGTGTAAAGATGACAAAGGTAGGGCAGTATGTTTAAATCAGACTTGGCAC	2220
Qy	2283	ATGGCTTAGGGAATCTGCTCACTAGCTGTGGAGGTCTTCAAGAGATGAGAGAAATAGTAG	2342
Dp	2221	ATGGCTTAGGGAATCTGCTCACTAGCTGTGGAGGTCTTCAAGAGATGAGAGAAATAGTAG	2280
Qy	2343	AGGGCAGAGGCTTCCATTTTGTGCTTCTPAAGACCGTAAATGATGATTAATTCCTGGC	2402
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Dp	2401	GAGGAACAAATTAGAACGTGGCAATGAGACCTGGCAGGGCAGAGTACAAAGCCACACCA	2460
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Qy	2883	ACAAGCTTGATAGGACGCCAATTTGTCTCTGGCCCTTGTGAGCACTCCGTGTGTGCT	2942
Dp	2821	ACAAGCTTGATAGGACGCCAATTTGTCTCTGGCCCTTGTGAGCACTCCGTGTGTGCT	2880
Qy	2943	GCCCTTCTCCCGCATAGCTGTGGGTCTGTGATGTGAAGATCGATGGGTTAACTG	3002
Dp	2881	GCCCTTCTCCCGCATAGCTGTGGGTCTGTGATGTGAAGATCGATGGGTTAACTG	2940
Qy	3003	TGTGCTTACTGAACCTGGCAATTAACATCACTTGCAAGCCAAATTAATTAATTAATTA	3062

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OY		3063	AAA 3065 	
Df		3001	AAA 3003	
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DEFINITION		Homo sapiens mRNA; cDNA DKFPZp686D0882 (from clone DKFPZp686D0882).		
ACCESSION		BX647074		
VERSION		BX647074.1	GI:34366102	
KEYWORDS				
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3176) Wambutt,S., Heubner,D., Mewes,H.W., weil,B., Amid,C., Oeanger,A., Fodor,G., Han,M. and Wiemann,S. The German Human cDNA Consortium Direct Submission Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuerberg, GERMANY		
CONSRMT		Neuberberg, GERMANY		
TITLE		Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.		
JOURNAL		This clone (DKFPZp686D0882) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cdna/ Location/Qualifiers		
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ORIGIN				
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Best Local Similarity		94.7%; Pred. No. 0;		
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OY		111	AGCGGATTTTCGCCCGCGCTGCCGGAAGCCCTCGGCGCCCGCTGAGCGCGATCACTTC	170
Df		61	AGCGGATTTTCGCCCGCGCTGCCGGAAGCCCTCGGCGCCCGCTGAGCGCGATCACTTC	120
OY		171	CTCCCTTGACAACACCGGCGCTGCAGGTTAGACCCTGAGCAATGCCGTTGGGTGTGAC	230
Df		121	CTCCCTTGACAACACCGGCGCTGCAGGTTAGACCCTGAGCAATGCCGTTGGGTGTGAC	180
OY		231	TCTGGGCGACAAGAAGAACTTAACCGAGCCATCGGAGTGACTGACGATTAATTTGGG	290
Df		181	TCTGGGCGACAAGAAGAACTTAACCGAGCCATCGGAGTGACTGACGATTAATTTGGG	240
OY		291	ACAGGTCACTCAAGACTGAGGAGTTTGTGAATCTTCGGGCGCAAAGGCAAGACGACAGG	350
Df		241	ACAGGTCACTCAAGACTGAGGAGTTTGTGAATCTTCGGGCGCAAAGGCAAGACGACAGG	300
OY		351	CACCTGTACACCTCTGCAAGAAGTTCCAGAACCGGAGCGGCCGCAAGGTGCGAAAGCTGC	410

Db 301 CAAGCTCACACCTGCAAGAAGTTCCAGAAAGCGGAGCGCGCAAGGTGCGGAAGCTGC 360
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 Db 361 CAAGAAGCATATGAGCATCTCTCAAGATGTGAGCATCCCAACATCTTACAGTGTGGA 420
 Qy 471 TGTGTTGTGACCCGCGAAGAGTACTTTATCTTCTGAGACTGGCCACGGGAGAGGT 530
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 Db 961 CTTTCAGGCAATCCACTTTCTATGAGAGGTGAGAAAGATGATATGAGAAACATGAT 1020
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 Db 1021 AAGAAATCTCTCCGCAAGATCTGTGCTGTGTGATGATGATGATGATGATGATGATGAT 1080
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QY	2410	GTCTCGAGGAGGCTGGCCCTGTGAACCTGGAACCTCATAGACCTCTTAAGGAAAGAGGAAC	2469
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QY	2470	AATTAGACGCTGGCAATGAGACTCTGCGACGGGACAGTACAAAGCCACAGACCCAGTGTCC	2529
Db	2581	AATTAGACGCTGGCAATGAGACTCTGCGACGGGACAGTACAAAGCCACAGACCCAGTGTCC	2640
QY	2530	AGCCTTACTGGGTCCTTAACCTGGGGCCAAACAGGGAAGGGCGATACCTCGTGTCTTCC	2589
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QY	2830	TCCCCAATTTTCCTAGAGGAGCTCTCAACAGTACCCCTTTGTCAAGCCCTTACCAACAGCT	2889
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QY	2890	GGATAGCAGCCACATTGATGTCCTGAGCCCTTGCTGCGACCTCCGTGATGTCCTGCCCTTC	2949
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QY	2950	TCCTCTGACGCTGTGGGTCTGCTCTGTGCTGTGTAAGTCCGTGGCTTAACTGTGTGCTCT	3009
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VERSION	AX086278.1	GI:13275924	
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
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REFERENCE	1
AUTHORS	Wiemann, S.
TITLE	Human dna sequences
JOURNAL	Patent: WO 0112659-A 230 22-FEB-2001;
	German Human Genome Project (DE)
FEATURES	Location/Qualifiers
SOURCE	1..2923

Query Match	90.4%	Score 2824.2	DB 6	Length 2923
Best Local Similarity	97.1%	Pred. NC 0		
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QY	589	CGGCAATCTCTGGAGGCGGTGCGCTATTTCGACTCATCAAGATCGGCAAGAACTCTC	648
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TITLE Direct Submission
JOURNAL Submitted (12-MAR-2002) MIPS, Am Klopferstr. 18a, D-82152 Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZ564E0482) is available at the RZPD in Berlin. Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.
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QY	1368	CACCCAGCCACAGATGAAGTGCACCCAGCACTGATGAGGATGCAACCCAGCCAC	1427	
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QY	1488	TACTCCAGCCACTGATGGGAGAGCCACACAGGCAAGAGAGACATGTGCCCACAC	1547	
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QY	1968	TGCTAGCTTCAACAGTTTCTGTCTTGTGAGATGCTCTTATAGGATATCTCAAGGGGCT	2027	
DB	1828	TGCTAGCTTCAACAGTTTCTGTCTTGTGAGATGCTCTTATAGGATATCTCAAGGGGCT	1887	

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coding sequence can be used as models for the development of human
therapeutic targets, in the identification of therapeutic proteins, and
serve as targets for the development of human therapeutic agents that
modulate kinase activity in cells and tissues that express the kinase. In
addition, the protein kinase coding sequence can be used for treating a
disorder associated with nucleic acid expression of the kinase gene,
particularly biological and pathological processes that are mediated by
the kinase in cells and tissues that express it, as antisense constructs
to control kinase gene expression in cells, tissues or organisms, and in
gene therapy. The protein kinase gene maps to chromosome 3

Sequence 3124 BP; 731 A; 861 C; 897 G; 635 T; 0 U; 0 Other;

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Db	1081	CAAGATGATGTGTGTGCGCAGATTTGAAGAAAGACTTTCGACAGGCGCAAGTGGAAAGGC	1140
QY	1158	TGTCCGAGTGAACACCTCTATTAACCGGCTCCGGGACCAAGACAGTCCAGACGGCTGC	1211
Db	1141	TGTCCGAGTGAACACCTCTATTAACCGGCTCCGGGACCAAGACAGTCCAGACGGCTGC	1200

QY	1218	AGCCCAAGTCGGCCCTCAGCCCAACAACATGCGACACCCCGGGGCTGAGAGTGGGGCAACAG	1277
Db	1201	AGCCCAAGTCGGCCCTCAGCCCAACAACATGCGACACCCCGGGGCTGAGAGTGGGGCAACAG	1260
QY	1278	TGCAGCTGCGAGTGGAGCTACCTCAGGCCCTGAGGGGTGATGCTGCTGCTCTGCAAGAG	1337
Db	1261	TGCAGCTGCGAGTGGAGCTACCTCAGGCCCTGAGGGGTGATGCTGCTGCTCTGCAAGAG	1320
QY	1338	TGATTAATGTGGCCCCCGCCAGACCCTAGTGGCACCCGACCAAGATGGAATGCGACCCC	1397
Db	1321	TGATTAATGTGGCCCCCGCCAGACCCTAGTGGCACCCGACCAAGATGGAATGCGACCCC	1380
QY	1398	AGCCACTGATGGCAGTGTCAACCCGACCCGATGGAAGCATCTCCAGCACTGATG	1457
Db	1381	AGCCACTGATGGCAGTGTCAACCCGACCCGATGGAAGCATCTCCAGCACTGATG	1440
QY	1458	GAGTGTCAACCCCACTGACAGAGGACGCTACTCCAGCCACTGATGGAGAGCGACACC	1517
Db	1441	GAGTGTCAACCCCACTGACAGAGGACGCTACTCCAGCCACTGATGGAGAGCGACACC	1500
QY	1518	AGCCACGAAGAGAGCACTGTGGCCACACACCMAAGCAGTGCATGTGTGCACCAAGGC	1577
Db	1501	AGCCACGAAGAGAGCACTGTGGCCACACACCMAAGCAGTGCATGTGTGCACCAAGGC	1560
QY	1578	AGCTGCCACCCCTCAGCGGGCTATGGCCAGCCGGAAGCAACGCCCAAGGGCGCAC	1637
Db	1561	AGCTGCCACCCCTCAGCGGGCTATGGCCAGCCGGAAGCAACGCCCAAGGGCGCAC	1620
QY	1638	AGGCCAGGCTCCACCTCTAGTAAAGGAGAAAGAGGCTGTGTGTTATGCCAGAGTCTCA	1697
Db	1621	AGGCCAGGCTCCACCTCTAGTAAAGGAGAAAGAGGCTGTGTGTTATGCCAGAGTCTCA	1680
QY	1698	AAAGGAGAGAGGCCACGCTGAGTAGAGCCACCTGTGTGAGGGGGGCGAGGGATGGCGAGAG	1757
Db	1681	AAAGGAGAGAGGCCACGCTGAGTAGAGCCACCTGTGTGAGGGGGGCGAGGGATGGCGAGAG	1740
QY	1758	GTGGGAGAGTGGATGAGGGGGCTTCTCACTGATACATAGAGTCACTGGGATGATGCTCTCG	1817
Db	1741	GTGGGAGAGTGGATGAGGGGGCTTCTCACTGATACATAGAGTCACTGGGATGATGCTCTCG	1800
QY	1818	TCCCCATGCCCCCACAATCCCACTGGGGCATTAATAGGAGGTCAACGGAGAGACGTCTGT	1877
Db	1801	TCCCCATGCCCCCACAATCCCACTGGGGCATTAATAGGAGGTCAACGGAGAGACGTCTGT	1860
QY	1878	CTCCTGTGTATGTGTGTGATGTGAGTGTGGGCAAGCCAGTGGCAGGGCGGGCCCCACCCCT	1937
Db	1861	CTCCTGTGTATGTGTGTGATGTGAGTGTGGGCAAGCCAGTGGCAGGGCGGGCCCCACCCCT	1920
QY	1938	GCAATGATTCCTTGTGGCTTTTCTGTCTTTTGTCTAGCTTCAACAGTTTCTGTCTCTGTG	1997
Db	1921	GCAATGATTCCTTGTGGCTTTTCTGTCTTTTGTCTAGCTTCAACAGTTTCTGTCTCTGTG	1980
QY	1998	GGAATGCTCTTAAGGATACTCAAGGGGGCTCTGCTCTTCCCTTCCCTTCTTGTGCT	2057
Db	1981	GGAATGCTCTTAAGGATACTCAAGGGGGCTCTGCTCTTCCCTTCCCTTCTTGTGCT	2040
QY	2058	CACCAATTCCTTAGGCAAGCCCTCAGGTCCCACTCTCCAGAGCCCTAAACTTGGCG	2117
Db	2041	CACCAATTCCTTAGGCAAGCCCTCAGGTCCCACTCTCCAGAGCCCTAAACTTGGCG	2100
QY	2118	GCTTTGCCCTGAGAGCTGTCTCTCCAGCAGAGCCCTGTCAAGCGTCTTAGGCTCTTGAC	2177
Db	2101	GCTTTGCCCTGAGAGCTGTCTCTCCAGCAGAGCCCTGTCAAGCGTCTTAGGCTCTTGAC	2160
QY	2178	ATGAAGGTGTGTGCTGTGTGTGTGTGGCTGTCTTAAGAGCAGATTAACAGGTGTGATAGA	2237
Db	2161	ATGAAGGTGTGTGCTGTGTGTGTGTGGCTGTCTTAAGAGCAGATTAACAGGTGTGATAGA	2220
QY	2238	GGATGCAAAAAGTATGGGCAAGATGTTAAATTCAGACTTGGCATATGGCTAGGAGTACT	2297
Db	2221	GGATGCAAAAAGTATGGGCAAGATGTTAAATTCAGACTTGGCATATGGCTAGGAGTACT	2280

154 GAGCCC-GCGATCACTTCTCCCTGTGACCAACCGGCGCTGCAGGTGAGACTGGACAT 212
122 GAGCCCGGCGATCACTTCTCTCTGTGACCAACCGGCGCTGCAGGTGAGACTGGACAT 181
213 GCGGTTTGGGTGTGTGACTCTGGGCGAGAGAGAACTTAACCAAGCCATCGAGGTGAC 272
182 GCGGTTTGGGTGTGTGACTCTGGGCGAGAGAGAACTTAACCAAGCCATCGAGGTGAC 241
213 TGACAGATATGATTTTGGGACAGGTCAATCAAGCTGAGAGATTTGTGAATCTTCCGGGC 332
242 TGACAGATATGATTTTGGGACAGGTCAATCAAGCTGAGAGATTTGTGAATCTTCCGGGC 301
333 CAGAGCAAGACGACAGGCAAGCTGCAACCTGCAAGAAATTTCCGAAGCGGAGCGCG 392
302 CAGAGCAAGACGACAGGCAAGCTGCAACCTGCAAGAAATTTCCGAAGCGGAGCGCG 361
393 CAGAGTGCAGAAAGCTGCAGAAAGAGATAGGCAATCTTCAAGATGTGAGACATCCCA 452
362 CAGAGTGCAGAAAGCTGCAGAAAGAGATAGGCAATCTTCAAGATGTGAGACATCCCA 421
453 CATCTTACAGCTGTGTGATGTGTGTGTGACCCGCAAGAGATCTTTATCTTCTGGAGCT 512
422 CATCTTACAGCTGTGTGATGTGTGTGTGACCCGCAAGAGATCTTTATCTTCTGGAGCT 481
513 GGCACAGGAGAGAGAGGTGTGTGACTGGATCTGTGACAGGCTATCTACTGAGAGCGAGA 572
482 GGCACAGGAGAGAGAGGTGTGTGACTGGATCTGTGACAGGCTATCTACTGAGAGCGAGA 541
573 CACAAGCAACGTGTGTATCGGCAAGCTCTGAGAGCGCTGTGCTATTTGGCACTCACTCAAT 632
542 CACAAGCAACGTGTGTATCGGCAAGCTCTGAGAGCGCTGTGCTATTTGGCACTCACTCAAT 601
633 CCTGCAACAGAAATCTCAAGCTGAGAGAACTGTGTACTTAACAACCGGCTGAGAACTCGAA 692
602 CCTGCAACAGAAATCTCAAGCTGAGAGAACTGTGTACTTAACAACCGGCTGAGAACTCGAA 661
693 GATTGTCAATCACTGATCTTCAATCTGGCTAAGCTAAGAAATGGCCTCATCAAGAGACCTGT 752
662 GATTGTCAATCACTGATCTTCAATCTGGCTAAGCTAAGAAATGGCCTCATCAAGAGACCTGT 721
753 TGGAGACCCCGAGATCTGTGCGCCAGAGGTGTATGGCGGCTATGACGCGCTGT 812
722 TGGAGACCCCGAGATCTGTGCGCCAGAGGTGTATGGCGGCTATGACGCGCTGT 781
813 GGAAGCTGTGGGCAATTTGAGATCATATGATCATCTGCTTCAAGGCAATCCACTTTCTA 872
782 GGAAGCTGTGGGCAATTTGAGATCATATGATCATCTGCTTCAAGGCAATCCACTTTCTA 841
873 TGAAGAGTGTGAAGAAAGATGATTAAGAGAACATGATAAGATCTCTTCCGCAAGACTCT 932
842 TGAAGAGTGTGAAGAAAGATGATTAAGAGAACATGATAAGATCTCTTCCGCAAGACTCT 901
933 GCGTGTGTGATATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 992
902 GCGTGTGTGATATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 961
993 CCGTGTGTGATATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 1052
962 CCGTGTGTGATATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 1021
1053 CTCCCATGAGTGAATTTCTGCGCAATGCTCTTCTGTAAGAACATCAAGATGTGTCTG 1112
1022 CTCCCATGAGTGAATTTCTGCGCAATGCTCTTCTGTAAGAACATCAAGATGTGTCTG 1081
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1082 TGCCAGATTGAAGAACTTTGCGAGGCGCAAGTGAAGAAAGGCTGTCCAGTGAACAAC 1141
1173 CCTCATGAAGACGGCTCCGGGCAACAAGAGTCAAGCAAGGCTGCAAGCCAGTCCGCTTC 1232
1142 CCTCATGAAGACGGCTCCGGGCAACAAGAGTCAAGCAAGGCTGCAAGCCAGTCCGCTTC 1201
1233 AGCCACAAGACACTGCAACCCCGGGGCTGAGGTGGGCGACAAGCTGCAAGTGGCAGATG 1292

1202 AGCCACAAGACACTGCCACCCCGGGGCTGCAGGTGGGCGACAAGCTGCAAGTGGCAGATG 1261
1293 AGCTACTTACGCCCCCTGAGGAGTATGCTGTCTGTCTGCATAAGATGATATGTGGCCCC 1352
1262 AGCTACTTACGCCCCCTGAGGAGTATGCTGTCTGTCTGCATAAGATGATATGTGGCCCC 1321
1353 CGGAGACGTTAGTCCACCCCGAGCCACAGATGGAAGTGCACCCGACCACTGATGGCAG 1412
1322 CGGAGACGTTAGTCCACCCCGAGCCACAGATGGAAGTGCACCCGACCACTGATGGCAG 1381
1413 TGTACCCCAAGCCACAGATGGAAGATCACTCAAGCCACTGAATGGAGTGTCAACCCAGT 1472
1382 TGTACCCCAAGCCACAGATGGAAGATCACTCAAGCCACTGAATGGAGTGTCAACCCAGC 1441
1473 CACTGACAGAGGCTACTTCAAGCCACTGATGGAGAGGCAACAAGCCACAAGAAAGAG 1532
1442 CACTGACAGAGGCTACTTCAAGCCACTGATGGAGAGGCAACAAGCCACAAGAAAGAG 1501
1533 CACTGTGCCCAACCAACCAAGAGAGTGCATGTGGTCAACAAAGGCAAGCTGCCACCCCTGA 1592
1502 CACTGTGCCCAACCAACCAAGAGAGTGCATGTGGTCAACAAAGGCAAGCTGCCACCCCTGA 1561
1593 GCGGCTATGGCCCAAGCCCGAGCAAGCAAGCCCAAGAGGCGGCAAGGCAAGGCTCAAC 1652
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1653 CTCTAGTAAAGGAGAAAGGCTGTCTGTATGCGCCAGAGTCTCAAGAGGAGAGGCGCAG 1712
1622 CTCTAGTAAAGGAGAAAGGCTGTGTATGCGCCAGAGTCTCAAGAGGAGAGGCGCAG 1681
1713 CTGAGTAAAGGAGGCTGTGAGAGGAGGAGAGGAGATGGGACAGAGAGGATGGAGATG 1772
1682 CTGAGTAAAGGAGGCTGTGAGAGGAGGAGAGGAGATGGGACAGAGAGGATGGAGATG 1741
1773 AGGAGCTTCTCATCTGTATCATATAGTCACTGGCATATGCTGCTTCCGCCATGCCCCA 1832
1742 AGGAGCTTCTCATCTGTATCATATAGTCACTGGCATATGCTGCTTCCGCCATGCCCCA 1801
1833 CATCCAGATGGGCGATATATGAGGAGTCAAGGAGAGACAGTCTGCTCGTGTGTATG 1892
1802 CATCCAGATGGGCGATATATGAGGAGTCAAGGAGAGACAGTCTGCTGTGTGTATG 1861
1893 GTGTAGTGTGTGGGCAAGGCGCAAGTGGAGGCGGCGCCCAAGCCCTGCATGATCCCTTG 1952
1862 GTGTAGTGTGTGGGCAAGGCGCAAGTGGAGGCGGCGCCCAAGCCCTGCATGATCCCTTG 1921
1953 GGCCTTTCGTCTTTCATGACTTCAACAGTTTCGTCTCTGTGGATGTGTCTGAG 2012
1922 GGCCTTTCGTCTTTCATGACTTCAACAGTTTCGTCTCTGTGGATGTGTCTGAG 1981
2013 GATATCAAGGAGGCTCTGTCTTCCCTTCCCTTCTGTGCTCAACATTCCTCTAG 2072
1982 GATATCAAGGAGGCTCTGTCTTCCCTTCCCTTCTGTGCTCAACATTCCTCTAG 2041
2073 CAGGCTCTGCAAGTCCCAACTCTTCCAGGCTTAACTTGGGCGGCTTGGCCTGAGAG 2132
2042 CAGGCTCTGCAAGTCCCAACTCTTCCAGGCTTAACTTGGGCGGCTTGGCCTGAGAG 2101
2133 CTGTCTCTCCAGAGGCGCTGTCAAGCGATCTTAAGCTCTCTGCAATGAAGTGTGTCC 2192
2102 CTGTCTCTCCAGAGGCGCTGTCAAGCGATCTTAAGCTCTCTGCAATGAAGTGTGTCC 2161
2193 TGTGTGTGTGGGTGTCTTAAGAGCAGATCAAGGCTGTGTATGAGAGTGCATAAAGGTA 2252
2162 TGTGTGTGTGGGTGTCTTAAGAGCAGATCAAGGCTGTGTATGAGAGTGCATAAAGGTA 2221
2253 GGGAGATATTTTAAGTCAAGACTTGGCAATGGCTTAAGGATCTGTCTCACTGAGCTGG 2312
2222 GGGAGATATTTTAAGTCAAGACTTGGCAATGGCTTAAGGATCTGTCTCACTGAGCTGG 2281
2313 AGGTCTCAGGAGTGAAGATGATGAGAGGAGAGAGCTTCAATTTTGTCTTCTCT 2372


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Db 2282 AGTCTCTCAGAGTGGAGAGATGATGAGAGGCGAGAGCTTCATTTCCTTCCT 2341
Qy 2273 AAGACCCCTGTTATTTGTTATTTTCCTGCCCTTCGAGTCCGTGAGTGGGCTGCCCTGTA 2432
Db 2342 AAGACCCCTGTTATTTGTTATTTTCCTGCCCTTCGAGTCCGTGAGTGGGCTGCCCTGTA 2401
Qy 2433 CCCTGAACTCATGAGCCTCTTAAAGGAAAGAGGAAACAATTAGACCTGGCAATGAGACC 2492
Db 2402 CCCTGAACTCATGAGCCTCTTAAAGGAAAGAGGAAACAATTAGACCTGGCAATGAGACC 2461
Qy 2493 TGGCAGGGCAGAGTCAAAAGCCAGACCCAGTGTCCAGCCTTACTGGGCTTCATCCCTG 2552
Db 2462 TGGCAGGGCAGAGTCAAAAGCCAGACCCAGTGTCCAGCCTTACTGGGCTTCATCCCTG 2521
Qy 2553 GGGCAAAACAGGAGGAGGCTGATACCTCCTTCCTTCCTTAATGCGCCACCTTCATCATCT 2612
Db 2522 GGGCAAAACAGGAGGAGGCTGATACCTCCTTCCTTCCTTAATGCGCCACCTTCATCATCT 2581
Qy 2613 CAGCCCAACAGTCTCTCCACCCCTAAGGGGGCTTGCTGCATGAGCAATACATCATATCTGA 2672
Db 2582 CAGCCCAACAGTCTCTCCACCCCTAAGGGGGCTTGCTGCATGAGCAATACATCATATCTGA 2641
Qy 2673 TTTGAGAGTTTGCCCTTACAGGGGAGATTTTCTGCTCAATTCAACATGAATGAGAGA 2732
Db 2642 TTTGAGAGTTTGCCCTTACAGGGGAGATTTTCTGCTCAATTCAACATGAATGAGAGA 2701
Qy 2733 GGAACCTCCCTTTCTTCAAGCTCACTTCTATCAGAGGCCAGAGTGCCTCAGAGCCACATT 2792
Db 2702 GGAACCTCCCTTTCTTCAAGCTCACTTCTATCAGAGGCCAGAGTGCCTCAGAGCCACATT 2761
Qy 2793 GAGTTGCTTTTCTTGGAGATGAGAGAGGTTAACTCCCAAGTTCCCTGAGGGAGGCT 2852
Db 2762 GAGTTGCTTTTCTTGGAGATGAGAGAGGTTAACTCCCAAGTTCCCTGAGGGAGGCT 2821
Qy 2853 CCTGACAGTGGCCCTTTGTGAGACCCCTACCAAGCCTGATGATGAGCAGCACAATTGGTCT 2912
Db 2822 CTTGACAGTGGCCCTTTGTGAGACCCCTACCAAGCCTGATGATGAGCAGCACAATTGGTCT 2881
Qy 2913 CGCCCTTGCTGGGCACTCCGTGATGATCTGCGCCCTTCCTGTGATGCTGTGGGTCTGC 2972
Db 2882 CGCCCTTGCTGGGCACTCCGTGATGATCTGCGCCCTTCCTGTGATGCTGTGGGTCTGC 2841
Qy 2973 TCTGAGTGTGAGAGTGGTGGGTTAACTGTGTCCTACTGAACTGGCAATTAACATC 3032
Db 2942 TCTGAGTGTGAGAGTGGTGGGTTAACTGTGTCCTACTGAACTGGCAATTAACATC 3001
Qy 3033 ACCCTGCAAGCCCAA 3048
Db 3002 ACCCTGCAAGCCCAA 3017

RESULT 4
ABX71280
ID ABX71280 standard; cDNA; 2923 BP.
AC ABX71280;
ABX71280;
DT 14-Apr-2003 (first entry)
XX Human signal transduction-associated cDNA from clone DKFzphf2_82e4.
XX Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
XX Homo sapiens.
XX W0200112659-A2.
XX W0200112659-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000MO-IB001456.
XX 18-AUG-1999; 99US-014949P.
XX 28-SEP-1999; 99US-0156503P.
PR
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XX (XEHU-) GERMAN HUMAN GENOME PROJECT.
PA
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
XX P-PSDB; ABUS2788.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies.
XX
XX Claim 1; Page 352-353; 1095bp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence encodes a polypeptide
CC described in the disclosure of the invention
XX
SQ Sequence 2923 BP; 644 A; 820 C; 849 G; 610 T; 0 U; 0 Other;

Query Match 90.4%; Score 2824.2; DB 5; Length 2923;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2920; Conservative 0; Mismatches 3; Indels 84; Gaps 1;

Qy 49 ATGCTGAGAGTTCCTGATACCCGAAGGCGCTGATCTGGGCGCGCTTCGCGCTGCTC 108
Db 1 ATGCTGAGAGTTCCTGATACCCGAAGGCGCTGATCTGGGCGCGCTTCGCGCTGCTC 60
Qy 109 GAGAGGAGATTTCGCCGCGCTGCCGAGAGCCCTCGAGCGCCCGCTGAGCCGCGATCACT 168
Db 61 GAGAGGAGATTTCGCCGCGCTGCCGAGAGCCCTCGAGCGCCCGCTGAGCCGCGATCACT 120
Qy 169 TCCTCCCTGTGACCAACCGCGCTGCAAGTTAAGCCTGAGATGCGCTTGGGTGTG 228
Db 121 TCCTCCCTGTGACCAACCGCGCTGCAAGTTAAGCCTGAGATGCGCTTGGGTGTG 180
Qy 229 ACTTGGGCGACAGAAATATTAACAGCCATCGAGGTGATGATGATATATTTG 288
Db 181 ACTTGGGCGTGAAGAAATATTAACAGCCATCGAGGTGATGATGATATATTTG 240
Qy 289 GAGACAGTTCATTAAGTGAAGAGTTTGTGAATCTTCCGGGCGCAAGACAAAGCGACA 348
Db 241 GAGACAGTTCATTAAGTGAAGAGTTTGTGAATCTTCCGGGCGCAAGACAAAGCGACA 300
Qy 349 GAGACAGTTCACACCTGCAAGAGTTTCAAGAGCGGAGCGCGCAAGGTGCGAAAGCT 408
Db 301 GAGACAGTTCACACCTGCAAGAGTTTCAAGAGCGGAGCGCGCGCAAGGTGCGAAAGCT 360
Qy 409 GCCAAGAAAGATAGGATCCTCAAGATGTGAAGATCCCAACATCTCAAGTGTG 468
Db 361 GCCAAGAAAGATAGGATCCTCAAGATGTGAAGATCCCAACATCTCAAGTGTG 420
Qy 469 GATGTGTTGTGACCCGCAAGAGTACTTTATCTTCTGTGAGCTGGCCAGCGGAGGGAG 528
Db 421 GATGTGTTGTGACCCGCAAGAGTACTTTATCTTCTGTGAGCTGGCCAGCGGAGGGAG 480
Qy 529 GGTGTTGACTGAGATCTGAGACGAGGCTACATCTCGAGCGAGACAGAAAGATGTGTA 588
Db 481 GGTGTTGACTGAGATCTGAGACGAGGCTACATCTCGAGCGAGACAGAAAGATGTGTA 540
Qy 589 CGGCAAGTCTGAGAGCGGCTGATTTGACTCACTCAAGATGTGACAGAGATCTC 648
Db 541 CGGCAAGTCTGAGAGCGGCTGATTTGACTCACTCAAGATGTGACAGAGATCTC 600
Qy 649 AAGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTGGAAGATTGTATCATGTGAC 708
Db 601 AAGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTGGAAGATTGTATCATGTGAC 660
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QY 709 TTCCATCTGAGCTAAGCTAGAAAAATGAGCTCATCAAGAGACCCCTGTGGACCCCGAGTAT 768
Db 661 TTCCATCTGAGCTAAGCTAGAAAAATGAGCTCATCAAGAGACCCCTGTGGACCCCGAGTAT 720
QY 769 CTGGCCCCAGAGGTGTAGAGCCGAGCGGATAGACCGCTGTGAGCTGTGGCCAT 828
Db 721 CTG----- 723
QY 829 GAGATCATGTACATCCCTGCTTCAAGCAATCCACCTTTCTATAGAGAGGTGAAAGA 888
Db 724 -----GGCAACCCACCTTTCTATAGAGAGGTGAAAGA 756
QY 889 GATGATTATAGAGAACCATGTATAGAACTCTTCGCAAGATCCTGTGCTGTGACTATAG 948
Db 757 GATGATTATAGAGAACCATGTATAGAACTCTTCGCAAGATCCTGTGCTGTGACTATAG 816
QY 949 TTGACTCTCCATATTTGGAGTATTTTGGCAGGCGCAAGACCTGTGTCACAAGGCTG 1008
Db 817 TTGACTCTCCATATTTGGAGTATTTTGGCAGGCGCAAGACCTGTGTCACAAGGCTG 876
QY 1009 ATGAGAGTGAAGAGACCAAGCGGATCACTGCAGAGAGGCCATCTCCATGATGTGATT 1068
Db -877 ATGAGAGTGAAGAGACCAAGCGGATCACTGCAGAGAGGCCATCTCCATGATGTGATT 936
QY 1069 TCTGGCAATGCTGCTTCTGTATAGAACTCAAGAGATGTGTCTGTGCCCAAGATTGAAA 1128
Db 937 TCTGGCAATGCTGCTTCTGTATAGAACTCAAGAGATGTGTCTGTGCCCAAGATTGAAA 996
QY 1129 AACTTTGCCAGGSCCAAGTGAAGAGAGGCTGTCCAGTGAACCACTCATGAAACGGCTC 1188
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QY 1249 ACCCGCGGAGCTGCAGAGTGGGAGCCACAGCTGCAGCTGCAGTGTGAGACTCTCTACGCC 1308
Db 1117 ACCCGCGGAGCTGCAGAGTGGGAGCCACAGCTGCAGCTGCAGTGTGAGACTCTCTACGCC 1176
QY 1309 GAGGAGTATGCTGCTGTGTGCAAGAGTATATGTGGCCCCGACACAGCTGTAGTGC 1368
Db 1177 GAGGAGTATGCTGCTGTGTGCAAGAGTATATGTGGCCCCGACACAGCTGTAGTGC 1236
QY 1369 ACCCGACACAGATGGAATGACACCCACGCCACTGATGGAGTGTCAACCCAGCCACC 1428
Db 1237 ACCCGACACAGATGGAATGACACCCACGCCACTGATGGAGTGTCAACCCAGCCACC 1296
QY 1429 GATGGAAGCATCTCCAGCCACTGATGGAGTGTCAACCCAGTCACTGACAGAGCGCT 1488
Db 1297 GATGGAAGCATCTCCAGCCACTGATGGAGTGTCAACCCAGTCACTGACAGAGCGCT 1356
QY 1489 ACTTCAGCCACTGATGGAGAGGCCACACAGCCACAGAGAGAGGACTGTGCCCAACACC 1548
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Db 1417 CAAGAGCATGCTGCTGAGCCACCAAGAGGAGCTGCCACCCCTGAGCGGCTATGAGCCAG 1476
QY 1609 CCGAGACGACAGAGCCCAAGAGGAGGAGCCACAGGCGCAGCTCACCTCTATGAAAGGAGA 1668
Db 1477 CCGAGACGACAGAGCCCAAGAGGAGGAGCCACAGGCGCAGCTCACCTCTATGAAAGGAGA 1536
QY 1669 GAGGCTGCTGTTATGCTCAGAGTCTCAAGAGAGAGGAGCCAGCTGATGAGGAGCTG 1728
Db 1537 GAGGCTGCTGTTATGCTCAGAGTCTCAAGAGAGAGGAGCCAGCTGATGAGGAGCTG 1596
QY 1729 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1788
Db 1597 GTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1656

QY 1789 ACATAGAGTCACTGGCATGATGCTCTGCTCCCATGCCCCACATCCCACTGGGAGCAT 1848
Db 1657 ACATAGAGTCACTGGCATGATGCTCTGCTCCCATGCCCCACATCCCACTGGGAGCAT 1716
QY 1849 AACTAGGAGTCAAGGAGAGAGTCTGCTCTGTGTGTATATGTGTGTGTGTGTGTGTGTGT 1908
Db 1717 AACTAGGAGTCAAGGAGAGAGTCTGCTCTGTGTGTATATGTGTGTGTGTGTGTGTGTGT 1776
QY 1909 GGCCAGTGGACGGGCGGGCCCAAGCCCTGACATGATTCCTGTGAGCTTCTGTCTTT 1968
Db 1777 GGCCAGTGGACGGGCGGGCCCAAGCCCTGACATGATTCCTGTGAGCTTCTGTCTTT 1836
QY 1969 GCTAGCTTCAACAGTTTCTGTCTTGTGGAGTGTGCTGTAGAGATCTCAAGGAGGCTC 2028
Db 1837 GCTAGCTTCAACAGTTTCTGTCTTGTGGAGTGTGCTGTAGAGATCTCAAGGAGGCTC 1896
QY 2029 CTGCTCTCTTCCCTTCCCTTCTGCTGTGCAATTCCTTAGGCAAGGCTGTGAGGCTC 2088
Db 1897 CTGCTCTCTTCCCTTCCCTTCTGCTGTGCAATTCCTTAGGCAAGGCTGTGAGGCTC 1956
QY 2089 CACACTCTCCAGGCTCTTAACCTTGGGCGGCTTGGCCCTGAGAGCTGTCTCCAGGAG 2148
Db 1957 CACACTCTCCAGGCTCTTAACCTTGGGCGGCTTGGCCCTGAGAGCTGTCTCCAGGAG 2016
QY 2149 GCCCTGTACGGGCTTAGGCTCCTGTGACATGAAAGTGTGTGCTGTGTGTGTGTGTGTG 2208
Db 2017 GCCCTGTACGGGCTTAGGCTCCTGTGACATGAAAGTGTGTGCTGTGTGTGTGTGTGTG 2076
QY 2209 CTCTAGAGCAGATACAGGCTGTGTATAGAGATGCAAGAAAGTATGAGGCAATGTTTAA 2268
Db 2077 CTCTAGAGCAGATACAGGCTGTGTATAGAGATGCAAGAAAGTATGAGGCAATGTTTAA 2136
QY 2269 TCCAGACTTGGCAGATGCTTAGGAGATCTGTCTACATGCTGTGTGAGGCTCTCAGAGT 2328
Db 2137 TCCAGACTTGGCAGATGCTTAGGAGATCTGTCTACATGCTGTGTGAGGCTCTCAGAGT 2196
QY 2329 AGAGATGAGTGAAGAGGAGGAGAGGCTTCAATTTTGTCTCTCTAGAACCTGTATTGT 2388
Db 2197 AGAGATGAGTGAAGAGGAGGAGAGGCTTCAATTTTGTCTCTCTAGAACCTGTATTGT 2256
QY 2389 TGTATTTCCTGCTTCCAGTCTCTGACAGTGGGCTGCTGTGACCTGTGACCTCATGAG 2448
Db 2257 TGTATTTCCTGCTTCCAGTCTCTGACAGTGGGCTGCTGTGACCTGTGACCTCATGAG 2316
QY 2449 CCTCTAAGAGAGAGAGAACATTTAGAGCGTGGCAATGAGCTGTGAGGCGCAGATAC 2508
Db 2317 CCTCTAAGAGAGAGAGAACATTTAGAGCGTGGCAATGAGCTGTGAGGCGCAGATAC 2376
QY 2509 AAGCCACAGACCCAGTGTCCAGGCTTACAGTGGCTTACCTGTGGGCAAGAGGAGG 2568
Db 2377 AAGCCACAGACCCAGTGTCCAGGCTTACAGTGGCTTACCTGTGGGCAAGAGGAGG 2436
QY 2569 CTGATACCTCTTCTCTCTAGATGCCACCTCTACATCTCAAGCCCAAGTCTC 2628
Db 2437 CTGATACCTCTTCTCTCTAGATGCCACCTCTCTACATCTCAAGCCCAAGTCTC 2496
QY 2629 TCCACCTTAGGAGGCTGTGCTGATGAGCAATCATTAATCTGATTTGAGGTTTGCCT 2688
Db 2497 TCCACCTTAGGAGGCTGTGCTGATGAGCAATCATTAATCTGATTTGAGGTTTGCCT 2556
QY 2689 TTAAGGAGGAGATTTTCTGCTCAGTTCAACATGAAATGAGAGAACTCCCTCTTCT 2748
Db 2557 TTAAGGAGGAGATTTTCTGCTCAGTTCAACATGAAATGAGAGAACTCCCTCTTCT 2616
QY 2749 ACAGCTCACTCTAATCAGAGGCGCAGGAGCTGAGAGCAATGAGTTGCTTTTCTG 2808
Db 2617 ACAGCTCACTCTAATCAGAGGCGCAGGAGCTGAGAGCAATGAGTTGCTTTTCTG 2676
QY 2809 GATGAGAGTATGAGTTTAACTCCCAATTTCTGAGAGGAGCTCTGACAGGAGCTCT 2868
Db 2677 GATGAGAGTATGAGTTTAACTCCCAATTTCTGAGAGGAGCTCTGACAGGAGCTCT 2736
QY 2869 TGTACAGCTTACCAACAGCTGTATGAGAGCCACATTTGCTCTGCGCTTCTCTGCGAC 2928
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Db 2737 TGTACACCCCTACACAGCCCTGTAGGACGACCATTTGTCTCGCCCTTGTCTCGCAC 2796
QY 2929 TCGGTGATGCTGCTGCTTCTCTCCCTGCANAGCTGTGGGTCTGTCTGTGTGAAAGG 2988
Db 2797 TCCGTGTGTGCTCTGCTCTCTCTCTCCCTGCANAGCTGTGGGTCTGTCTGTGTGAAAGG 2856
QY 2989 CGGTGGTTAACTGTGTGCTTGAACCTTGCAATTAACATCACTTGCACAAAGCCAA 3048
Db 2857 CGGTGGTTAACTGTGTGCTTGAACCTTGCAATTAACATCACTTGCACAAAGCCAA 2916
QY 3049 AAAAAA 3055
Db 2917 AAAAAA 2923

RESULT 5
AAK94325
ID AAK94325..standard; cDNA: 2905 BP.

XX AC AAK94325;

XX DT 06-NOV-2001 (first entry)

XX DE Human full-length cDNA, SEQ ID NO: 3007.

XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX OS Homo sapiens.

XX PN EP1130094-A2.

XX PD 05-SEP-2001.

XX PE 07-JUL-2000; 2000EP-00114089.

XX PR 08-JUL-1999; 99JP-00194486.

XX PR 11-JAN-2000; 2000JP-00118774.

XX PR 02-MAY-2000; 2000JP-00183765.

XX PA (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Iehi S, Kawai Y,

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WP1; 2001-524255/58.

DR P-PSDB; AAM93404.

XX PT 830 Primers useful for synthesizing full length cDNA clones and their use

XX in genetic manipulation.

XX PS Claim 8; SEQ ID NO 3007; 1380bp + Sequence Listing; English.

XX CC The invention relates to primers for synthesizing full length cDNA

XX clones. 830 cDNA molecules encoding a human protein have been isolated

XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

XX been determined. Primers for synthesizing the full length cDNA are useful

XX for clarifying the function of the protein encoded by the cDNA. The full

XX length clones were obtained by construction of full length enriched cDNA

XX libraries that were synthesized by the oligo-capping method. The primers

XX enable the production of the full length cDNA easily without any special

XX methods. The present sequence is a full length human cDNA of the

XX invention. Note: The sequence data for this patent did not form part of

XX the printed specification, but was obtained in CD-ROM format directly

XX from EPO

XX SQ Sequence 2905 BP; 630 A; 819 C; 846 G; 610 T; 0 U; 0 Other;

XX Query Match 89.4%; Score 2792.4; DB 4; Length 2905;

XX Best Local Similarity 96.7%; Pred. No. 0;

XX Matches 2899; Conservative 0; Mismatches 6; Indels 93; Gaps 1;

Db 1 GATGTGTGAAGGTTCCCTTATGCGAAGCCGCTCATCTGTGCGCGGTCTGCCCCGGTCT 60
QY 108 CGGAGCGGATTTCTGCCCCCGCTCCCGAGGCGCTCGAGCGCCCGCTGAGCCGCGATCAC 167
Db 61 CGGAGCGGATTTCTGCCCCCGCTCCCGAGGCGCTCGAGCGCCCGCTGAGCCGCGATCAC 120
QY 168 TTCTCTCCCTGTGACCAACCGCGCTGACAGTTAGAGCTTGCCTTGTGGTGTGT 227
Db 121 TCCCTCTCCCTGTGACCAACCGCGCTGACAGTTAGAGCTTGCCTTGTGGTGTGT 180
QY 228 GACTCTGCGCGACAAAGAAAGAACTATTAACCAAGCATCGAGGTGACTGACAGATGATTT 287
Db 181 GACTCTGCGGTGACAAAGAAAGAACTATTAACCAAGCATCGAGGTGACTGACAGATGATTT 240
QY 288 GGGACAGGTCATCAAGACTGAGAGAGTTTGTGAATCTTCGCGGCGCAAGACAGAC 347
Db 241 GGGACAGGTCATCAAGACTGAGAGAGTTTGTGAATCTTCGCGGCGCAAGACAGAC 300
QY 348 AGGCAAGCTGCACACCTGCAAGAAAGTTCCAGAGCGGAGCGCGCAAGCTGCGGAAAGC 407
Db 301 AGGCAAGCTGCACACCTGCAAGAAAGTTCCAGAGCGGAGCGCGCAAGCTGCGGAAAGC 360
QY 408 TCCCAAGAAAGAGATAGGCAATCTCAAGATGTGAGAGATCCCAATCTTACAGCTGGT 467
Db 361 TCCCAAGAAAGAGATAGGCAATCTCAAGATGTGAGAGATCCCAATCTTACAGCTGGT 420
QY 468 GGAATGTTTGTGACCCCGAAGAGATTAATCTTCTGAGCTGCGACCGGAGGGA 527
Db 421 GGAATGTTTGTGACCCCGAAGAGATTAATCTTCTGAGCTGCGACCGGAGGGA 480
QY 528 GGTGTTTGAATCTGGAATCTTGGACCAAGGCTTACTCTCGAGAGGAGACAAAGCAAGTGT 587
Db 481 GGTGTTTGAATCTGGAATCTTGGACCAAGGCTTACTCTCGAGAGGAGACAAAGCAAGTGT 540
QY 588 AGGCAAGCTGCACACCTGCAAGAAAGTTCCAGAGCGGAGCGCGCAAGCTGCGGAAAGC 647
Db 541 AGGCAAGCTGCACACCTGCAAGAAAGTTCCAGAGCGGAGCGCGCAAGCTGCGGAAAGC 600
QY 648 CAAGCTGAGAAACCTGGTTTACTTACCAACCGGCTGAAGAACTTGAATTCATCAGTGA 707
Db 601 CAAGCTGAGAAACCTGGTTTACTTACCAACCGGCTGAAGAACTTGAATTCATCAGTGA 660
QY 708 CTTCCATCTGCGCTAAGCTTGAAGAAATGGCTTCATCAAGAGCCCTGTGGAGCCCGGAGTA 767
Db 661 CTTCCATCTGCGCTAAGCTTGAAGAAATGGCTTCATCAAGAGCCCTGTGGAGCCCGGAGTA 720
QY 768 TCTGGGCCAGAGGAGGTATAGGCGGAGCGGATGAGAGCCCTGTGAGCTGTGGAGCAT 827
Db 721 TCTGGGCCAGAGGAGGTATAGGCGGAGCGGATGAGAGCCCTGTGAGCTGTGGAGCAT 780
QY 828 TGAAGCATCATGATCATCTGCTTTACAGGCAATCCACTTTCTATGAGAGGTGAAAG 887
Db 781 TGAAGCATCATGATCATCTGCTTTACAGGCAATCCACTTTCTATGAGAGGTGAAAG 840
QY 888 AGATGATTAAGAAACCATGATTAAGAAATCTTCCGCAAGATCTGTGGCTGTGACTATGA 947
Db 841 AGATGATTAAGAAACCATGATTAAGAAATCTTCCGCAAGATCTGTGGCTGTGACTATGA 900
QY 948 GTTTGACTCTCCATATTTGGAGATGATTTTTCGAGGACCAAGACCTGTGACAGAGGT 1007
Db 901 GTTTGACTCTCCATATTTGGAGATGATTTTTCGAGGACCAAGACCTGTGACAGAGGT 960
QY 1008 GATGAGGTGAGAGCAGAACCAAGGATCATCTGCAAGAGGCGCATCTCCATGATGAT 1067
Db 961 GATGAGGTGAGAGCAGAACCAAGGATCATCTGCAAGAGGCGCATCTCCATGATGAT 1020
QY 1068 TTCTGGCATGTGCTTCTGTATAGAAACATCAAGATGTGTCTGTGCGCAGATTAAGAA 1127
Db 1021 TTCTGGCATGTGCTTCTGTATAGAAACATCAAGATGTGTCTGTGCGCAGATTAAGAA 1080
QY 1128 GAACTTGTCCAGGCGCAAGTGAAGAGGCTGTCCGATGACCACTTCATGTAAGACGCT 1187

Db	1081	GAACCTTTGCCAGGGGCCAAGTGGAGAAAGGCTGTCCAGTGAACACCTCATGAAACGGCT	1140
QY	1188	CCGGGCAACCAAGCAGTTCACAGCAGGCTGCAGCCAGTCGGCTTCAGCCACAGACACTGC	1247
Db	1141	CCGGGCAACCAAGCAGTTCACAGCAGGCTGCAGCCAGTCGGCTTCAGCCACAGACACTGC	1200
QY	1248	CACCCCCGGGGCTGTCAGTGGGGGCCAAGCTGCAGCTGCAGTGGAGCTACTCAAGCCCC	1307
Db	1201	CACCCCCGGGGCT-----	1213
QY	1308	TGAGGTGTAGTCTCTCGTGTGCAGAAAGTGAATGTGGCCCCCGAGACCGTAGTGC	1367
Db	1214	-----GCAAGCCGTATGTC	1227
QY	1368	CACCCCAAGCCACAGATGGAATGTCACCCCAAGCTGATGGCAGTGTCACCCCAGCCAC	1427
Db	1228	CACCCCAAGCCACAGATGGAATGTCACCCCAAGCTGATGGCAGTGTCACCCCAGCCAC	1287
QY	1428	CGATGGAAAGCATCACTCCAGCCACTGATGGGAAGTGTCACCCCAGTCACTGACAGAGAGCC	1487
Db	1288	CGATGGAAAGCATCACTCCAGCCACTGATGGGAAGTGTCACCCCAGTCACTGACAGAGAGCC	1347
QY	1488	TACTCCAGCCCTGATGGGAGAGGCCACACAGGCCACAGAAAGAGCACTGTGGCCACAC	1547
Db	1348	TACTCCAGCCCTGATGGGAGAGGCCACACAGGCCACAGAAAGAGCACTGTGGCCACAC	1407
QY	1548	CCAAAGCAGTGCATGTCTGCGCCACCAAGGAGCACTGCCACCCCTAGAGCCGCTATAGGCCCA	1607
Db	1408	CCAAAGCAGTGCATGTCTGCGCCACCAAGGAGCACTGCCACCCCTAGAGCCGCTATAGGCCCA	1467
QY	1608	GCCGGAACGACACAGGCCCGAGGGCGCCACAGGCCAGCTTCACCTCTAGTAAAGGGGA	1667
Db	1468	GCCGGAACGACACAGGCCCGAGGGCGCCACAGGCCAGCTTCACCTCTAGTAAAGGGGA	1527
QY	1668	AGAGGCTGTCTGCTTATGTCCCAAGAGTCTCAAAAGGAGAGGCCAGCTGATAGTAAAGCAGCT	1727
Db	1528	AGAGGCTGTCTGCTTATGTCCCAAGAGTCTCAAAAGGAGAGGCCAGCTGATAGTAAAGCAGCT	1587
QY	1728	GGTAGGGGGGGGCGAGGGATGAGCGAGAGGGTGGGAGATGGAGGGGCTTCTCACTG	1787
Db	1588	GGTAGGGGGGGGCGAGGGATGAGCGAGAGGGTGGGAGATGGAGGGGCTTCTCACTG	1647
QY	1788	TACATAGAGTCACTGGCANTGATGCCCTTGCTCCCCATGAGCCCCCAATCCCAAGTGGGGCA	1847
Db	1648	TACATAGAGTCACTGGCANTGATGCCCTTGCTCCCCATGAGCCCCCAATCCCAAGTGGGGCA	1707
QY	1848	TAACTAGGGGGTCAACGGAGAGCAAGTCTGTCTCTGTGTGATGTGTGTAGTGGTGGCC	1907
Db	1708	TAACTAGGGGGTCAACGGAGAGCAAGTCTGTCTCTGTGTGATGTGTGTAGTGGTGGCC	1767
QY	1908	AGGCAAGTGGAGGGGCGGGCCCGAGGCCCTGCAATGGAATTCCTGTGTGGCTTTTCTCTT	1967
Db	1768	AGGCAAGTGGAGGGGCGGGCCCGAGGCCCTGCAATGGAATTCCTGTGTGGCTTTTCTCTT	1827
QY	1968	TGCTAGCTTCAACAATTCTGTCTCTTGTGGGATGCTGCTAGAGATACACAGGGGCT	2027
Db	1828	TGCTAGCTTCAACAATTCTGTCTCTTGTGGGATGCTGCTAGAGATACACAGGGGCT	1887
QY	2028	CTGTGCTCTCTCCCTTCCCTTCTTCTGCTCAACATTCCTCCCTAGCAGGCGCTTCAGGTC	2087
Db	1888	CTGTGCTCTCTCCCTTCCCTTCTTCTGCTCAACATTCCTCCCTAGCAGGCGCTTCAGGTC	1947
QY	2088	CCACACTTCCCAAGGCGCTTAACTTGGGCGGCTTGCCCTGAGAGCTGTCTCCAAGGA	2147
Db	1948	CCACACTTCCCAAGGCGCTTAACTTGGGCGGCTTGCCCTGAGAGCTGTCTCCAAGGA	2007
QY	2148	GAGCCTGTCAAGGGGTCTTAGGCTCTGCACATGAAGTGTGTGCTGTGTGTGTGGGCT	2207
Db	2008	GAGCCTGTCAAGGGGTCTTAGGCTCTGCACATGAAGTGTGTGCTGTGTGTGTGGGCT	2067
QY	2208	GCTTAGAGAGCAGATACAGGCTGTATAGAGATCAGAAAGGTAGGCGATGTATTAA	2267

Qy	2268	GTCCAGCTTGGCACAATGGCTTAGGAAATCTGCTCACTAGTGTGGAGTCTCTCAGAGAGTG	2327
Db	2128	GTCACAGCTTGGCACAATGGCTTAGGAAATCTGCTCACTAGTGTGGAGTCTCTCAGAGAGTG	2187
Qy	2328	GAGAGATGAGTGGAGAGGGCAGAAAGCTTCCATTTTTGTCTTCTCTAGAACCTGTATTT	2387
Db	2188	GAGGAAATGAGTAGAGAGGGCAGAAAGCTTCCATTTTTGTCTTCTCTAGAACCTGTATTT	2247
Qy	2388	GGTGTATTTCTCGCTTTCCGAGTCTCGAGTGGGCTGCCCTGTACCTTGAACCTCATGA	2447
Db	2248	GTGTATTTCTCGCTTTCCGAGTCTCGAGTGGGCTGCCCTGTACCTTGAACCTCATGA	2307
Qy	2448	GCCCTTAAGGAAAGAGGAAACAATTGAGACGTGGGAAATGAAACCTGGCAGGGGAGAGTA	2507
Db	2308	GCCCTTAAGGAAAGAGGAAACAATTGAGACGTGGGAAATGAAACCTGGCAGGGGAGAGTA	2367
Qy	2508	CAAGCCACGACACCGAGTGTCCAGCCTTAATGGGTCTTACCCCTGGGCCAAACAGGAGG	2567
Db	2368	CAAGCCACGACACCGAGTGTCCAGCCTTAATGGGTCTTACCCCTGGGCCAAACAGGAGG	2427
Qy	2568	GCTGATACCTGCTTGTCTTCTTAGATGCCACCTCTCAATCTACGCCCAAGTCTT	2627
Db	2428	GCTGATACCTGCTTGTCTTCTTAGATGCCACCTCTCAATCTACGCCCAAGTCTT	2487
Qy	2628	CTCACACCTTAGGGGSCCTTGTGTCAGATGGCAATTAATCTAATCTGATTTGGAGTTTGGCC	2687
Db	2488	CTCACACCTTAGGGGSCCTTGTGTCAGATGGCAATTAATCTAATCTGATTTGGAGTTTGGCC	2547
Qy	2688	TTTACAGGGGACAGATTTTCTGCTCAGTTTCAACAATGAATGAAGAGAGACTCCCTCTTTC	2747
Db	2548	TTTACAGGGGACAGATTTTCTGCTCAGTTTCAACAATGAATGAAGAGAGACTCCCTCTTTC	2607
Qy	2748	TACAGCTCACTTCTATCAGAGGCCACAGTGCCTCAGAGCAACATTGATTTCTTTTCTG	2807
Db	2608	TACAGCTCACTTCTATCAGAGGCCACAGTGCCTCAGAGCAACATTGATTTCTTTTCTG	2667
Qy	2808	GGATGAGAAATAGAGCTTAAATCCCAAGTTTCTGAGGAGAGGCTCCTGACAGGTGACCT	2867
Db	2668	GGATGAGAAATAGAGCTTAAATCCCAAGTTTCTGAGGAGAGGCTCCTGACAGGTGACCT	2727
Qy	2868	TTGTCAAGACCTTACACAGGCTGTGATGAGACACATTGTGCTCCGCTTGTCTCGCA	2927
Db	2728	TTGTCAAGACCTTACACAGGCTGTGATGAGACACATTGTGCTCCGCTTGTCTCGCA	2787
Qy	2928	CTCCGTGGTGTCTGCTGCCCTTCTCCCTGCATGCTGTGGGTCTGCTCTGGTGTGAAG	2987
Db	2788	CTCCGTGGTGTCTGCTGCCCTTCTCCCTGCATGCTGTGGGTCTGCTCTGGTGTGAAG	2847
Qy	2988	TCCGTGGTGTATCTGTGTGCTTATGAAACCTGGCAAATTAACATCAACCTGCAAGGC	3045
Db	2848	TCCGTGGTGTATCTGTGTGCTTATGAAACCTGGCAAATTAACATCAACCTGCAAGGC	2905
RESULT 6			
AA158144			
ID AA158144 standard; cDNA; 2840 BP.			
XX AA158144;			
XX 22-OCT-2001 (first entry)			
XX DE Human polynucleotide SEQ ID NO 347.			
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;			
KW peripheral nervous system; neuropathy; central nervous system; CNS;			
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;			
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;			
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;			
XX leukemia; ss.			

PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSB-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX P-PSDB; AAM38988.
XX
XX Novel nucleic acid and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Claim 1; SEQ ID NO 347; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression.
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemia and
XX CC C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
SQ Sequence 2840 BP; 619 A; 795 C; 834 G; 592 T; 0 U; 0 Other;
Query Match 89.3%; Score 2791.2; DB 4; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 50 TGTCTGAGAGTTCCCTGACCGGAGCGGCTGATCTGGCGCCGCTGCCCCGCTGCTG 109
DB 45 TGTCTGAGAGTTCCCTGACCGGAGCGGCTGATCTGGCGCCGCTGCCCCGCTGCTG 104
QY 110 GAGCGGAGTTTGTGCGCCGCGCTGCGGAGCGCTGGGCGCCCGGTGAGCCCGGATGACTT 169
DB 105 GAGCGGAGTTTGTGCGCCGCGCTGCGGAGCGCTGGGCGCCCGGTGAGCCCGGATGACTT 164
QY 170 CCTTCCCTGTGACCAACGCGCGCTGAGGTTAGAGCTGTGCAATGCGGTTGGTGTGTGA 229
DB 165 CCTTCCCTGTGACCAACGCGCGCTGAGGTTAGAGCTGTGCAATGCGGTTGGTGTGTGA 224
QY 230 CTTTGGGCGAGCAAGAAAGTATTAACGAGCATCGAGGTGACTGACAGATATGATTTGG 289
DB 225 CTTTGGGCGAGCAAGAAAGTATTAACGAGCATCGAGGTGACTGACAGATATGATTTGG 284
QY 290 GACAGGTCATCAGAGCTGAGAGAGTTTGTGAAATCTTCCGGGCGAAGACAAAGACAG 349
DB 285 GACAGGTCATCAGAGCTGAGAGAGTTTGTGAAATCTTCCGGGCGAAGACAAAGACAG 344
QY 350 GCAAGTCGACACCTGCAAGAGTTTCCAGAAAGCGGAGCGCCGCAAGTGTCGGAAAGCTG 409

DB 345 GCAAGTCGACACCTGCAAGAGTTTCCAGAAAGCGGAGCGCCGCAAGTGTCGGAAAGCTG 404
QY 410 CCAAGAACGAGATAGGCAATCTCTCAAGATGTTGAAGCATCTCCCAAGTCTCTACAGTGTGG 469
DB 405 CCAAGAACGAGATAGGCAATCTCTCAAGATGTTGAAGCATCTCCCAAGTCTCTACAGTGTGG 464
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QY 530 TGTTTGACTGTGATCTGTGACCAAGGAGTACTACTGAGCGAGACACAAGAACCTGTGTAC 589
DB 525 TGTTTGACTGTGATCTGTGACCAAGGAGTACTACTGAGCGAGACACAAGAACCTGTGTAC 584
QY 590 GCAAGTCCTGAGAGCGCGTGCGCTATTGGACTGCACTCAAGATGTCAGAGAACTTCA 649
DB 585 GCAAGTCCTGAGAGCGCGTGCGCTATTGGACTGCACTCAAGATGTCAGAGAACTTCA 644
QY 650 AGCTGAGAAACCTGCTTTACTTACTCAACCGGCTGGAAGAACTGGAATGTTCATGATGACT 709
DB 645 AGCTGAGAAACCTGCTTTACTTACTCAACCGGCTGGAAGAACTGGAATGTTCATGATGACT 704
QY 710 TCCATCTGCTAGCTAGAAATAGGCTCATCAAGAGAGCCCTGTGGAGCCCGGAGTATC 769
DB 705 TCCATCTGCTAGCTAGAAATAGGCTCATCAAGAGAGCCCTGTGGAGCCCGGAGTATC 764
QY 770 TGGCCCGAGAGTGTAGAGCGCGGAGGATATGACCGCTGTGAGACTGTGGCCCATTTG 829
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QY 830 GAGTCATCATATACATCTCTGTTTCAAGCAATCCACTTTTATGAGAGGTGGAAGAG 889
DB 825 GAGTCATCATATACATCTCTGTTTCAAGCAATCCACTTTTATGAGAGGTGGAAGAG 884
QY 890 ATGATTTAGAAACCATGATTAAGAAATCTTCCGCAAGTCCCTGGCTGTGATATGATAGT 949
DB 885 ATGATTTAGAAACCATGATTAAGAAATCTTCCGCAAGTCCCTGGCTGTGATATGATAGT 944
QY 950 TTGACTCTCCATTTATGGGATGATATTTTCGAGAGCGCAAGAAAGCTGTGCAAGAGCTGA 1009
DB 945 TTGACTCTCCATTTATGGGATGATATTTTCGAGAGCGCAAGAAAGCTGTGCAAGAGCTGA 1004
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DB 1005 TGAAGTGAAGCAAGACCAAGCGGATCACTGCAAGAGAGCCATCTCCATGATGATTT 1064
QY 1070 CTGGCAATGCTGCTTCTGTGATTAAGAAATCAAGATGCTGTGTGCTGCTGCAAGTGAAGA 1129
DB 1065 CTGGCAATGCTGCTTCTGTGATTAAGAAATCAAGATGCTGTGTGCTGCTGCAAGTGAAGA 1124
QY 1130 ACTTTGCCAGGGCCAGAGTGAAGAGGCTGTGCGAGTGAACCAACCTCATGAAAGGGCTCC 1189
DB 1125 ACTTTGCCAGGGCCAGAGTGAAGAGGCTGTGCGAGTGAACCAACCTCATGAAAGGGCTCC 1184
QY 1190 GGGGACCAAGACAGTTCAGACAGGCTGCAAGCCAGTGGGCTTCAGACACAGACTGCGCA 1249
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QY 1250 CCCCCGGGGCTGCAAGTGGGGCCACAGCTGAGCTGCGAGTGAAGCTTACCTCAGCCCTTG 1309
DB 1245 CCCCCGGGGCTGCAAGTGGGGCCACAGCTGAGCTGCGAGTGAAGCTTACCTCAGCCCTTG 1304
QY 1310 AGGGTGAATGCTGCTGTGCTGCTGCAAGAGTATATGTGTGCCCCCGGACAGACCTGTGCA 1369
DB 1305 AGGGTGAATGCTGCTGTGCTGCTGCAAGAGTATATGTGTGCCCCCGGACAGACCTGTGCA 1364
QY 1370 CCCCAGCCACAGATGGAAGAGTGCACCCAGCCATGATGAGAGTGTACACCCAGCCACCG 1429
DB 1365 CCCCAGCCACAGATGGAAGAGTGCACCCAGCCATGATGAGAGTGTACACCCAGCCACCG 1424
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QY 1490 CTCACGCCCATGTATGGAGAGCCACACCAAGCCACAGAAAGAGACCTGTGCCACACACCC 1549
Db 1485 CTCACATCCATGATGGGATGAGCCACACCAAGCCAGAAAGAGACCTGTGCCACACACCC 1544
QY 1550 AAAGAGATGCCATGTGGCCACCAAGAGAGCTGCACCCCTGAGCCGGCTATGGCCAGC 1609
Db 1545 AAAGAGATGCCATGTGGCCACCAAGAGAGCTGCACCCCTGAGCCGGCTATGGCCAGC 1604
QY 1610 CGGACAGCAGAGCCCAAGAGAGGCGCCACAGGCGCTCCACCTCTATGAAAGGAGAG 1669
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QY 1730 TGAAGGGGGGAGAGGAGTGGGAGAGAGGGTGGGAGAGTGGAGAGGGGCTTCTCACTGA 1789
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Db 1785 CATAGAGTCACTGGGCTATGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1844
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QY 1910 GCCAGTGGGAGAGGCGCGGCGCCAGCCCTGATGAGATCTTGTGGCTTTCTGCTTTTG 1969
Db 1905 GCCAGTGGGAGAGGCGCGGCGCCAGCCCTGATGAGATCTTGTGGCTTTCTGCTTTTG 1964
QY 1970 CTAGGCTTACCAAGTTCTGTTCTGTTGGGATGCTGCTAGAGGATACCTCAGGGGCTCC 2029
Db 1965 CTAGGCTTACCAAGTTCTGTTCTGTTGGGATGCTGCTAGAGGATACCTCAGGGGCTCC 2024
QY 2030 TGGCTCTCTCCCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2089
Db 2025 TGGCTCTCTCCCTTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2084
QY 2090 ACACTCTCCAGGCGCTTAAACTTGGGCGGCTTGGCTGAGAGCTGCTGCTGCTGCTGCTG 2149
Db 2085 ACACTCTCCAGGCGCTTAAACTTGGGCGGCTTGGCTGAGAGCTGCTGCTGCTGCTGCTG 2144
QY 2150 CCTGTGACGGGCTTAAAGGCTCTGCAATGAAAGTGTGCTGCTGCTGCTGCTGCTGCTG 2209
Db 2145 CCTGTGACGGGCTTAAAGGCTCTGCAATGAAAGTGTGCTGCTGCTGCTGCTGCTGCTG 2204
QY 2210 TCTAGAGCAGATACAGGCTGATATAGAGATGACAGAAAGTATGAGGCACTATGTTAGT 2269
Db 2205 TCTAGAGCAGATACAGGCTGATATAGAGATGACAGAAAGTATGAGGCACTATGTTAGT 2264
QY 2270 CCAGACTTGGCAGATGAGTATGAGATCTGCTCACTAGCTGTGAGAGTCTCTCAGAGTGA 2329
Db 2265 CCAGACTTGGCAGATGAGTATGAGATCTGCTCACTAGCTGTGAGAGTCTCTCAGAGTGA 2324
QY 2330 GAGAAATGATGAGAGGAGAGAGCTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTTCTT 2389
Db 2325 GAGAAATGATGAGAGGAGAGAGCTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTTCTT 2384
QY 2390 GTATATTTCCGCTTTCCAGATCTGCAAGTGGGCTGCCCTGTAACCTGTAACCTGTAAGC 2449
Db 2385 GTATATTTCCGCTTTCCAGATCTGCAAGTGGGCTGCCCTGTAACCTGTAACCTGTAAGC 2444
QY 2450 CTCTAAGGAGAGAGAGAGCAATTAAGACGTGCAATGAGACCTGCGAGGAGAGTACA 2509
Db 2445 CTCTAAGGAGAGAGAGAGCAATTAAGACGTGCAATGAGACCTGCGAGGAGAGTACA 2504
QY 2510 AGCCCAAGCAGCAGTGTCCAGGCTTATCTGGTCTTACCTTGGGCAAAACAGGGAGGCG 2569
Db 2505 AGCCCAAGCAGCAGTGTCCAGGCTTATCTGGTCTTACCTTGGGCAAAACAGGGAGGCG 2564

QY 2570 TGATACCTCTCTGCTCTCTCTGATGATGCCAGCCCTTACATCTCAGCCCAAGTCTCT 2629
Db 2565 TGATACCTCTCTGCTCTCTCTGATGATGCCAGCCCTTACATCTCAGCCCAAGTCTCT 2624
QY 2630 CCACCTTATGGGAGCTTGTGCTGATGAGCAATPACTGATATCTGATTTGAGGTTTGCCCTT 2689
Db 2625 CCACCTTATGGGAGCTTGTGCTGATGAGCAATPACTGATATCTGATTTGAGGTTTGCCCTT 2684
QY 2690 TACAGGGGAGATTTTCTGCTCAGTTCAACATGAAATGAAAGAGAACTCCCTTTCTTA 2749
Db 2685 TACAGGGGAGATTTTCTGCTCAGTTCAACATGAAATGAAAGAGAACTCCCTTTCTTA 2744
QY 2750 CAGCTCACTTCTATCAAGAGGCGCAGGCTCAGAGCCACATTTAGATTGCTTTTCTGGG 2809
Db 2745 CAGCTCACTTCTATCAAGAGGCGCAGGCTCAGAGCCACATTTAGATTGCTTTTCTGGG 2804
QY 2810 ATGAGGAGTATGAGGTTAACTCCCAAGTTTCTGAG 2845
Db 2805 ATGAGGAGTATGAGGTTAACTCCCAAGTTTCTGAG 2840

RESULT 7
ADB48110
ID ADB48110 standard; cDNA; 2840 BP.
XX
AC ADB48110;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 20.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PE 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
XX
PR 25-APR-2000; 2000US-00552317.
XX
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX
XX
DR WPI; 2003-678194/64.
XX
PT New polynucleotide, useful for treating diseases e.g., cancer or
XX neurodegenerative diseases.
PS
XX Claim 1; SEQ ID NO 20; 99PP; English.
XX
CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docid=20030104529.
XX
SQ Sequence 2840 BP; 619 A; 795 C; 834 G; 592 T; 0 U; 0 Other;
Query Match 89.3%; Score 2791.2; DB 8; Length 2840;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY TGCTGAGGTTCCGTACCCGAAAGGGCTGATCTGGGCGCGCTGCCCCGGTGTCTG 109
Db TGCTGAGGTTCCGTACCCGAAAGGGCTGATCTGGGCGCGCTGCCCCGGTGTCTG 104
QY 110 GAGGAGATTCTGCCCCGCGTCCCGAGCCCTGGCGCCCGCGTGAAGCCCGCATCTT 169
Db 105 GAGGAGATTCTGCCCCGCGTCCCGAGCCCTGGCGCCCGCGTGAAGCCCGCATCTT 164
QY 170 CCTCCCTGTGACCAACCGCGCTGCAAGCTTGAAGCTTGAAGCTTGGTGTGTGA 229
Db 165 CCTCCCTGTGACCAACCGCGCTGCAAGCTTGAAGCTTGAAGCTTGGTGTGTGA 224
QY 230 CTCTGGGCGACAGAAATCTATACAGCCATGGAGGTGACTGACATGATGATTTGG 289
Db 225 CTCTGGGCGACAGAAATCTATACAGCCATGGAGGTGACTGACATGATGATTTGG 284
QY 290 GACAGCTCATCAGACTGAGAGTTTGTGAATCTTCCGGGCGAAGAACAGACAGCAG 349
Db 285 GACAGCTCATCAGACTGAGAGTTTGTGAATCTTCCGGGCGAAGAACAGACAGCAG 344
QY 350 GCAAGCTGCAACCTGCAAGAGTTCCAGAACCGGACCGGCAAGGTGCGGAAGCTG 409
Db 345 GCAAGCTGCAACCTGCAAGAGTTCCAGAACCGGACCGGCAAGGTGCGGAAGCTG 404
QY 410 CCAAGAACAGATAGGATCTCTCAAGATGATGAACATCCCAATCTCAAGCTGTGG 469
Db 405 CCAAGAACAGATAGGATCTCTCAAGATGATGAACATCCCAATCTCAAGCTGTGG 464
QY 470 ATGTGTTTGTGACCCGCAAGAGATCTTATCTTCTGAGCTGGCCACCGGAGGAGG 529
Db 465 ATGTGTTTGTGACCCGCAAGAGATCTTATCTTCTGAGCTGGCCACCGGAGGAGG 524
QY 530 TGTGTACTGGATCTGAGACAGAGGCTACTACTGAGGCGAGACAGAAAGAGGTGTAC 589
Db 525 TGTGTACTGGATCTGAGACAGAGGCTACTACTGAGGCGAGACAGAAAGAGGTGTAC 584
QY 590 GGCAGACTCTGAGAGCGGTGCTATTGCACTCACTCAAGATCGTCAAGAGATCTCA 649
Db 585 GGCAGACTCTGAGAGCGGTGCTATTGCACTCACTCAAGATCGTCAAGAGATCTCA 644
QY 650 AGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTGGAAGTTGTATCATGACT 709
Db 645 AGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTGGAAGTTGTATCATGACT 704
QY 710 TCCATCTGGCTAAGACTAGAAAATGGCTCATCAAGAGCCCTGTGGGACCCCGAGTATC 769
Db 705 TCCATCTGGCTAAGACTAGAAAATGGCTCATCAAGAGCCCTGTGGGACCCCGAGTATC 764
QY 770 TGGCCCAAGAGGTGTAGGCGCGAGCGGATAGGAGCCCGTGGAGCTGCTGGGCAATG 829
Db 765 TGGCCCAAGAGGTGTAGGCGCGAGCGGATAGGAGCCCGTGGAGCTGCTGGGCAATG 824
QY 830 GAGTCATCATGTACATCTGCTTCAAGCAATCCACTTTCTATGAGAGGTGAGAGAG 889
Db 825 GAGTCATCATGTACATCTGCTTCAAGCAATCCACTTTCTATGAGAGGTGAGAGAG 884
QY 890 ATGATTAAGAACCATGATTAAGATCTTTCGCAAGATCTGCTGTGACTATGAGT 949
Db 885 ATGATTAAGAACCATGATTAAGATCTTTCGCAAGATCTGCTGTGACTATGAGT 944
QY 950 TTGACTCTCCATATTGGAGATATTTCGAGAGAGGCAAGACTGTGTCACAAAGGTGA 1009
Db 945 TTGACTCTCCATATTGGAGATATTTCGAGAGAGGCAAGACTGTGTCACAAAGGTGA 1004
QY 1010 TGGAGGTGAGACAGACGAGGATCACTGCAAGAGGCAATCTCCATGAGTGTATTT 1069
Db 1005 TGGAGGTGAGACAGACGAGGATCACTGCAAGAGGCAATCTCCATGAGTGTATTT 1064
QY 1070 CTGGCAATGCTGCTTGTGATTAAGACATCAAGATGTGTGTGTGCCAGATTGAAAGA 1129

Db 1065 CTGGCAATGCTGCTTGTGATTAAGACATCAAGATGTGTGTGTGCCAGATTGAAAGA 1124
QY 1130 ACTTTGCCAGGGCCCAAGTGAAGAAAGGTGTCCAGATGACCAACCTCATGAAACGGCTCC 1189
Db 1125 ACTTTGCCAGGGCCCAAGTGAAGAAAGGTGTCCAGATGACCAACCTCATGAAACGGCTCC 1184
QY 1190 GGGCACACAGAGATCTCAGACAGCGGTGCAAGCCAGTCGGGCTCTAGCCACAGACTGCGCA 1249
Db 1185 GGGCACACAGAGATCTCAGACAGCGGTGCAAGCCAGTCGGGCTCTAGCCACAGACTGCGCA 1244
QY 1250 CCCCCGGGCTGCAAGTGGGCGCAACGCTGACGAGTGAAGCTACCTCAGCCCTTG 1309
Db 1245 CCCCCGGGCTGCAAGTGGGCGCAACGCTGACGAGTGAAGCTACCTCAGCCCTTG 1304
QY 1310 AGGTGATGCTGCTGTGTCTGCAAGATGATTAATGTGTGCCCCCGCAGACCGTATGCGCA 1369
Db 1305 AGGTGATGCTGCTGTGTCTGCAAGATGATTAATGTGTGCCCCCGCAGACCGTATGCGCA 1364
QY 1370 CCCCAGCCAGATGGAAGTGCACCCAGCCACTGATGGAGTGTACCCCGACGCAAG 1429
Db 1365 CCCCAGCCAGATGGAAGTGCACCCAGCCACTGATGGAGTGTACCCCGACGCAAG 1424
QY 1430 ATGGAAGATCACTCAGCCACTGATGGAGTGTACCCAGTCACTGACAGAGCGCTA 1489
Db 1425 ATGGAAGATCACTCAGCCACTGATGGAGTGTACCCAGTCACTGACAGAGCGCTA 1484
QY 1490 CTCACGCCATGATGGAGAGGCCACACAGCCACAGAAAGAGCACTGTGCCACCAACC 1549
Db 1485 CTCACGCCATGATGGAGAGGCCACACAGCCACAGAAAGAGCACTGTGCCACCAACC 1544
QY 1550 AAGAGATGCCATGTGTGCCACCAAGGCAAGTCCCAACCCCTGAGCGGCTATGGCCACG 1609
Db 1545 AAGAGATGCCATGTGTGCCACCAAGGCAAGTCCCAACCCCTGAGCGGCTATGGCCACG 1604
QY 1610 GGAAGACAGAGCCCGAGAGGCGGCCACAGGCGAGGCTCCACCCCTCTAGTAAAGGGAG 1669
Db 1605 GGAAGACAGAGCCCGAGAGGCGGCCACAGGCGAGGCTCCACCCCTCTAGTAAAGGGAG 1664
QY 1670 AGGCTGCTGTTATCCAGAGAGTCTCAAGAGGAGAGGCGAGCTGATGAGAGGCTG 1729
Db 1665 AGGCTGCTGTTATCCAGAGAGTCTCAAGAGGAGAGGCGAGCTGATGAGAGGCTG 1724
QY 1730 TGAAGGGGGGCGAGGATGGGCGAGAGGAGTGGAGATGAGAGGCTTCTCACTGTA 1789
Db 1725 TGAAGGGGGGCGAGGATGGGCGAGAGGAGTGGAGATGAGAGGCTTCTCACTGTA 1784
QY 1790 CATAGATCATGTGAGATGATGCTTCTGCTCCCCCATGCCCCCATCTCCAGTGGGCACTA 1849
Db 1785 CATAGATCATGTGAGATGATGCTTCTGCTCCCCCATGCCCCCATCTCCAGTGGGCACTA 1844
QY 1850 ACTAGGGGCTACGGAGAGAGTCTGCTCTGCTGTGATGATGATGATGATGATGATG 1909
Db 1845 ACTAGGGGCTACGGAGAGAGTCTGCTCTGCTGTGATGATGATGATGATGATGATG 1904
QY 1910 GCCAGTGGAGGGCGGGCCAGCCAGCCCTGATGATGATGATGATGATGATGATG 1969
Db 1905 GCCAGTGGAGGGCGGGCCAGCCAGCCCTGATGATGATGATGATGATGATGATG 1964
QY 1970 CTAGCTTACCAAGTTTCTGTTCTTGTGGAGTGTGCTCTAGAGGATCTCAGGGGCTCC 2029
Db 1965 CTAGCTTACCAAGTTTCTGTTCTTGTGGAGTGTGCTCTAGAGGATCTCAGGGGCTCC 2024
QY 2030 TGTCTCTCTCCCTTCCCTTCTGCTTCTGCTCAATCCCTTGGGCGAGGCGCTGAGGTC 2089
Db 2025 TGTCTCTCTCCCTTCCCTTCTGCTTCTGCTCAATCCCTTGGGCGAGGCGCTGAGGTC 2084
QY 2090 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGTGCTGAGAGCTGTCTCTCAGCGAGG 2149
Db 2085 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGTGCTGAGAGCTGTCTCTCAGCGAGG 2144
QY 2150 CCTGTACAGCGGCTTAAAGCTTCTGCAATGAAGGTGTGTGCTGTGTGTGTGTGTG 2209
Db 2145 CCTGTACAGCGGCTTAAAGCTTCTGCAATGAAGGTGTGTGCTGTGTGTGTGTGTG 2204

QY 2210 TCTAGAGAGAGATACAGGCTGGTATAGAGATGACAGAAAGGTAGGGACATGTTAAGT 2269
DB 2205 TTTAGAGAGAGATACAGGCTGGTATAGAGATGACAGAAAGGTAGGGACATGTTAAGT 2264
QY 2270 CCAGACTTGGACATGGCTAGGAGATATGCTGCTAGTGTGAGAGTCTCAGAGATGGA 2339
DB 2265 CCAGACTTGGACATGGCTAGGAGATATGCTGCTAGTGTGAGAGTCTCAGAGATGGA 2324
QY 2330 GAGATAGATAGAGAGGACGAAAGCTTCCATTTTGTCTCTCTAAGACCTGTTATTTGT 2389
DB 2325 GAGATAGATAGAGAGGACGAAAGCTTCCATTTTGTCTCTCTAAGACCTGTTATTTGT 2384
QY 2390 GTTATTTCTGCTTCCGAGTCTGAGTGGGCTGGCTGGCTGACCTGACCTGATGAGC 2449
DB 2385 GTTATTTCTGCTTCCGAGTCTGAGTGGGCTGGCTGGCTGACCTGATGAGC 2444
QY 2450 CTCTAAGGAGAAAGAGAAACAATTAGACGTGGCATGAGACCTGGCAGGCGAGATACA 2509
DB 2445 CTCTAAGGAGAAAGAGAAACAATTAGACGTGGCATGAGACCTGGCAGGCGAGATACA 2504
QY 2510 AGCCGACAGCCAGATGTCCAGCCTTACTGGTCTTACCTGGGCCAAAGAGAGGC 2569
DB 2505 AGCCGACAGCCAGATGTCCAGCCTTACTGGTCTTACCTGGGCCAAAGAGAGGC 2564
QY 2570 TGAATACCTCTGCTCTTCTTGAATGCCACCTCTCAATCTGAGCCCAAGTCTCT 2629
DB 2565 TGAATACCTCTGCTCTTCTTGAATGCCACCTCTCAATCTGAGCCCAAGTCTCT 2624
QY 2630 CCACCTTAGGGGGCTTGTGATGAGCAATTAATCTGATTGAGGTTGCGCTT 2689
DB 2625 CCACCTTAGGGGGCTTGTGATGAGCAATTAATCTGATTGAGGTTGCGCTT 2684
QY 2690 TACAGGGGAGATTTTCTGCTCAGTTCAACAATGAATGAAGAGAACTCCCTCTTCTA 2749
DB 2685 TACAGGGGAGATTTTCTGCTCAGTTCAACAATGAATGAAGAGAACTCCCTCTTCTA 2744
QY 2750 CAGCTCAGTTCTATCAGAGGCCCGAGGTGCTCAGAGCCACATTTGCTTTTCTGCG 2809
DB 2745 CAGCTCAGTTCTATCAGAGGCCCGAGGTGCTCAGAGCCACATTTGCTTTTCTGCG 2804
QY 2810 ATGAGAGAGATAGGTTAAACTCCCGAGTTTCTCTGAG 2845
DB 2805 ATGAGAGAGATAGGTTAAACTCCCGAGTTTCTCTGAG 2840

RESULT 8

AA30481 ID AAF30481 standard; cDNA, 2897 BP.
XX AAF30481;
XX
XX
XX 29-MAY-2001 (first entry)
DE Human protein phosphatase and kinase protein-6 cDNA 1385073CB1.
XX
XX Protein phosphatase and kinase protein; PPHK-6; human;
KM Gastrointestinal disorder; immune system disorder; neurological disorder;
KM cell proliferative disorder; cancer; diagnosis; therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 149..1561
FT /+tag= a
FT /+tag= b
FT /note= "unique fragment"
FT misc_feature 1298..1357
FT /+tag= c
FT /note= "unique fragment"
XX
XX
XX WO200120004-A2.

XX 22-MAR-2001.
XX
XX 14-SEP-2000; 2000MO-US025515.
XX
XX 15-SEP-1999; 99US-0154141P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Tang YT, Bandman O, Hillman JL, Baughn MR, Azimzai Y;
PI Lu DM;
PI
XX
XX WPI; 2001-244811/25.
DR P-PSDB; AAB20327.
XX
XX Novel human protein phosphatase and kinase proteins for diagnosis,
PT treatment and prevention of gastrointestinal, immune system, neurological
PT and cell proliferative disorders.
XX
XX Claim 5; Page 99; 103pp; English.
XX
XX The present sequence is that of cDNA encoding novel human protein
CC phosphatase and kinase protein PPHK-6 (see AAB20327). The cDNA was
CC initially identified in Incyte Clone ID No. 1385073CB1, from a brain
CC tumour tissue library. Tissues that express PPHK-6 (as a fraction of
CC total tissues expressing PPHK-6) include nervous (0.885) and
CC developmental (0.077). Diseases or conditions associated with tissues
CC expressing PPHK-6 (as a fraction of total tissues expressing PPHK-6)
CC include inflammation or trauma (0.384), neurological (0.231) and cancer
CC (0.192). The encoded protein shows homology to rat calmodulin-binding
CC protein. The invention provides human PPHK-1 to -11 polypeptides (see
CC AAB20322-32) and polynucleotides (see AAB30476-86). It also provides
CC expression vectors, host cells, antibodies, agonists and antagonists, as
CC well as methods for diagnosing, treating or preventing disorders
CC associated with expression of PPHK, including gastrointestinal
CC disorders, immune system disorders, neurological disorders and cell
CC proliferative disorders, including cancer
XX
XX Sequence 2897 BP; 636 A; 816 C; 838 G; 607 T; 0 U; 0 Other;
SQ
Query Match 89.3%; Score 2790.8; DB 4; Length 2897;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 2; Indels 93; Gaps 1;
QY 63 CTAGCCGAGCGGCTGATGCGCGCGCTGCGCCCGGCTGCTGAGCGGATTTCTGC 122
DB 1 CTAGCCGAGCGGCTGATGCGCGCGCTGCGCCCGGCTGCTGAGCGGATTTCTGC 60
QY 123 CCGCGCTCCCGGAGCCCTTGCGCGCCCGGCTGAGCGCGGATTTCTGC 182
DB 61 CCGCGCTCCCGGAGCCCTTGCGCGCCCGGCTGAGCGCGGATTTCTGC 120
QY 183 AACCGGCGTGGAGGTTAGAGCCCTGCGCAATGCCGTTTGGGTGCTGCGCGCA 242
DB 121 AACCGGCGTGGAGGTTAGAGCCCTGCGCAATGCCGTTTGGGTGCTGCGCGCA 180
QY 243 GAAGAATATTAACAGGCGATCGAGGTGACTGACATATGATTTGGGACAGGTCA 302
DB 181 GAAGAATATTAACAGGCGATCGAGGTGACTGACATATGATTTGGGACAGGTCA 240
QY 303 GACTGAGAGTTTGTGAAATCTTCGCGGCGAAGAGACAGACAGGCAAGTGCAC 362
DB 241 GACTGAGAGTTTGTGAAATCTTCGCGGCGAAGAGACAGGCAAGTGCAC 300
QY 363 CTGCAAGAGTTTCCAGAGCGGAGCGCCGCAAGGTGCGGAAAGCTGCCAAGAGAT 422
DB 301 CTGCAAGAGTTTCCAGAGCGGAGCGCCGCAAGGTGCGGAAAGCTGCCAAGAGAT 360
QY 423 AGGATCTCTCAAGATGAGAGCATCCCAATCTCTCAAGCTGATGATGTTGAGC 482
DB 361 AGGATCTCTCAAGATGAGAGCATCCCAATCTCTCAAGCTGATGATGTTGAGC 420
QY 483 CCGCAAGAGTACTTATCTTCTGAGCTGCGCCAGCGGAGGAGGTGTTGACTGGAT 542

Db		421	CCGGAAGGAGTACTTTCCTTCCTGGAAGCTGGCCACGGGAGAGGAGGTTTGA	CTGAT	480
Qy		543	CTTGGACCAAGGGCTACTACCTGGAGCGAGACA	CAAGCAACGTGTATCGGACAGTCTTGA	602
Db		481	CTGGACCAAGGGCTACTACTGGAGCGAGACA	CAAGCAACGTGTATCGGACAGTCTTGA	540
Qy		603	GGCGGTGGCTTATTTTGACTCACTCTA	AATGTGTGACAGAAATCTCAAGCTTGAAGAACTT	662
Db		541	GGCGGTGGCTTATTTTGACTCACTCTA	MAATGTGTGACAGAAATCTCAAGCTTGAAGAACTT	600
Qy		663	GGTTTACTACAAACGGGTGAAGAACTG	GAAGTTGTTCATCATGTGACTTCCATCTGGCTAA	722
Db		601	GGTTTACTACAAACGGGTGAAGAACTG	GAAGTTGTTCATCATGTGACTTCCATCTGGCTAA	660
Qy		723	GCTAAGAAATGGCTCATCAAGAGACCCCTGTGGGA	CCCCCGAGTACTTGGCCCCGAGAGT	782
Db		661	GCTAAGAAATGGCTCATCAAGAGACCCCTGTGGGA	CCCCCGAGTACTTGGCCCCGAGAGT	720
Qy		783	GGTAGCCCGGACGGGTATGGAACGCTCTGTGGACTGT	GGGCCATTTGAGATCATATGTA	842
Db		721	GGTAGCCCGGACGGGTATGGAACGCTCTGTGGACTGT	GGGCCATTTGAGATCATATGTA	780
Qy		843	CATCCTGCTTTCAGGCAATTCACCTTTTCTATGAGAG	GGTGGAGAAAGTATATGAGAA	902
Db		781	CATCCTGCTTTCAGGCAATTCACCTTTTCTATGAGAG	GGTGGAGAAAGTATATGAGAA	840
Qy		903	CCATGATTAAGATCTCTTCGCAAGATCCTGAGTGA	CTATGAGTTTGACTCTCCATA	962
Db		841	CCATGATTAAGATCTCTTCGCAAGATCCTGAGTGA	CTATGAGTTTGACTCTCCATA	900
Qy		963	TTGGGATGATATTTGSCAGAGCAGCCAAAGACTGT	GTCAAGAGCTGATGAGAGTGAAGCA	1022
Db		901	TTGGGATGATATTTGSCAGAGCAGCCAAAGACTGT	GTCAAGAGCTGATGAGAGTGAAGCA	960
Qy		1023	AGACCAAGGGATCACTGTCAGAAAGGCCATCT	CCCATAGTGATTTCTGGCAATGCTGC	1082
Db		961	AGACCAAGGGATCACTGTCAGAAAGGCCATCT	CCCATAGTGATTTCTGGCAATGCTGC	1020
Qy		1083	TTCTGATTAAGAACTCAAGAGATGGGTGTGTG	CCCCAGATTGAAAAGACTTGGCAAGGC	1142
Db		1021	TTCTGATTAAGAACTCAAGAGATGGGTGTGTG	CCCCAGATTGAAAAGACTTGGCAAGGC	1080
Qy		1143	CAAGTGAAGAGGCTGTCCAGATGACACACT	CTATGAAAGGCTCCGGGACAGAGACA	1202
Db		1081	CAAGTGAAGAGGCTGTCCAGATGACACACT	CTATGAAAGGCTCCGGGACAGAGACA	1140
Qy		1203	GTCCAAGCAGGCTGACGCCAGTGGGCTTACAG	CCACACTGCGACCCCGGGGCTGC	1262
Db		1141	GTCCAAGCAGGCTGACGCCAGTGGGCTTACAG	CCACACTGCGACCCCGGGGCTGC	1198
Qy		1263	AGGTGGGGCCACAGTGTGACGTGCGAGTGAAG	CTCAACCCCTGAGGGTATGCTGC	1322
Db		1199	-----	-----	1198
Qy		1323	TCTGTGCTCAAGAAGTGAATATGTGGCCCG	CAGACCGTATGTCACCCCAAGCAAGA	1382
Db		1199	-----	-----	1382
Qy		1383	TGGAAGTCCACCCAGCCTGATGGCAGTGTCA	CCCCAGCCACCGATGGAAAGATCAC	1442
Db		1228	TGGAAGTCCACCCAGCCTGATGGCAGTGTCA	CCCCAGCCACCGATGGAAAGATCAC	1287
Qy		1443	TTCAAGCACTATGGAGATGTCACTCCCACTCA	CTGACAGAGCGCTACTCAAGCCACTGA	1502
Db		1288	TTCAAGCACTATGGAGATGTCACTCCCACTCA	CTGACAGAGCGCTACTCAAGCCACTGA	1347
Qy		1503	TGGGAGAGCCCAACAGCCACAGAAAGAAAG	CACTGTGCCACCAACCAAGCAAGTGCAT	1562
Db		1348	TGGGAGAGCCCAACAGCCACAGAAAGAAAG	CACTGTGTGCCACCAACCAAGCAAGTGCAT	1407
Qy		1563	GCTGGCCACCAAGGACGTGCACCCCTGAGC	CGGCTATTTGGCCAGCCGAGCAGACAGC	1622

Db	1408	GCTGGCCACCAAGGACACTGCAACCCCTGAGCGGCGTATGGCCGACGCCGACACACAGC	1467
QY	1623	CCGAGAGGGGCCCAACAGGCGCAGGCTCCACCCCTCTAGTAAAGGGGAGAAGAGCTGCTGGTTA	1682
Db	1468	CCGAGAGGGGCCCAACAGGCGCAGGCTCCACCCCTCTAGTAAAGGGGAGAAGAGGCTGCTGGTTA	1527
QY	1683	TGCCCCAGAGCTCTAAAGGAGAGGGCCAGCTGATAGGCAGCCTGGTGAAGGGGGGGCAG	1742
Db	1528	TGCCCAAGAGCTCTAAAGGAGAGGGCCAGCTGATAGGCAGCCTGGTGAAGGGGGGGCAG	1587
QY	1743	GGAGTGGGCAAGAGGGGTGGGAGAGTGGATGAGGGGGCTTCCACTGTATCATATGATGCACTG	1802
Db	1588	GGAGTGGGCAAGAGGGGTGGGAGAGTGGATGAGGGGGCTTCCACTGTATCATATGATGCACTG	1647
QY	1803	GCATGATGCCCCGCTCCCTCCCAATGCCCAATCCAGTGGGGCATTAATTAGGGGTACAG	1862
Db	1648	GCATGATGCCCCGCTCCCTCCCAATGCCCAATCCAGTGGGGCATTAATTAGGGGTACAG	1707
QY	1863	GGAGAGCAGTCTGCTCTCTGTGTGTATGTGTGTAGTGGTGGCAGGCCAGTGGCAGGG	1922
Db	1708	GGAGAGCAGTCTGCTCTCTGTGTGTGTGTGTGTAGTGGTGGCAGGCCAGTGGCAGGG	1767
QY	1923	CGGGCCCCAGCCCCCTGATGGATTCCTATGGGCTTTCTGTCTTTAGTACTTACACAG	1982
Db	1768	CGGGCCCCAGCCCCCTGATGGATTCCTATGGGCTTTCTGTCTTTAGTACTTACACAG	1827
QY	1983	TTTCTGTCTCTGTGGAGTGTGCTCTAGGGATATCTACAGGGGGCTCTGCTCTCTCTCC	2042
Db	1828	TTTCTGTCTCTGTGGAGTGTGCTCTAGGGATATCTACAGGGGGCTCTGCTCTCTCTCC	1887
QY	2043	CTTCCCTTCTTGCTCAACATTCCTCCCTAGGAGGCGCTGCAGAGTCCCACTCTCCAGG	2102
Db	1888	CTTCCCTTCTTGCTCAACATTCCTCCCTAGGAGGCGCTGCAGAGTCCCACTCTCCAGG	1947
QY	2103	CCCTTAACTTGGGGGGGCTTGCCCTGAGAGCTGGTCTCCAGCGAGGCGCTGTACAGGGGT	2162
Db	1948	CCCTTAACTTGGGGGGGCTTGCCCTGAGAGCTGGTCTCCAGCGAGGCGCTGTACAGGGGT	2007
QY	2163	CTTAAAGCTCCCTGCACATGAAAGGTGTGGCTGTGTGTGGGGTGGCTCTAGAGAGCAGAT	2222
Db	2008	CTTAAAGCTCCCTGCACATGAAAGGTGTGTGGCTGTGTGTGGGGTGGCTCTAGAGAGCAGAT	2067
QY	2223	ACAGGCTGTATAGAGAGATGCAGAAAGTATAGGCGAGTATGTTTAAGTCCAGACTTGGCAC	2282
Db	2068	ACAGGCTGTATAGAGAGATGCAGAAAGTATAGGCGAGTATGTTTAAGTCCAGACTTGGCAC	2127
QY	2283	ATGGCTTAAAGGATTAAGTCTCACTAGCTGTGAAGTCTCTCAGAGATGGAGAGATAGTAGG	2342
Db	2128	ATGGCTTAAAGGATTAAGTCTCACTAGCTGTGAAGTCTCTCAGAGATGGAGAGATAGTAGG	2187
QY	2343	AGGCGACAAGCTTCATTTTGTGCTCTTAAGACCGTGTATTTGTGTTATTTCTGCGC	2402
Db	2188	AGGCGACAAGCTTCATTTTGTGCTCTTAAGACCGTGTATTTGTGTTATTTCTGCGC	2247
QY	2403	TTTTCGAGTCCCTGCAGTGGGCTGGCTGCTACCTCGAACCCTCATATGAGCCTCTAAGGAAAG	2462
Db	2248	TTTTCGAGTCCCTGCAGTGGGCTGGCTGCTACCTCGAACCCTCATATGAGCCTCTAAGGAAAG	2307
QY	2463	GAGGACAATTAGGACGTGGCAATGAGACTGTGCAGGGGCGAGTATCAAGCCAGCACCCA	2522
Db	2308	GAGGACAATTAGGACGTGGCAATGAGACTGTGCAGGGGCGAGTATCAAGCCAGCACCCA	2367
QY	2523	GTGTCCCAAGCTTATCTGGGTCTTAACTCTGGGCCAACAAGGAGGGGTGATATCTCTTG	2582
Db	2368	GTGTCCCAAGCTTATCTGGGTCTTAACTCTGGGCCAACAAGGAGGGGTGATATCTCTTG	2427
QY	2583	CTTCTCCAGATGGCCCACTCTCATATCTCAGGCCCAAGTCCCTCTCCACCCTAAGGGGG	2642
Db	2428	CTTCTCCAGATGGCCCACTCTCTCATATCTCAGGCCCAAGTCCCTCTCTCCACCCTAAGGGGG	2487
QY	2643	CTTCTCCAGATGGCAATAACTCATATATCTGATTTTGGAGTTTGGCCCTTATCAAGGGGCAAT	2702
Db	2488	CTTCTCCAGATGGCAATAACTCATATATCTGATTTTGGAGTTTGGCCCTTATCAAGGGGCAAT	2547

Db 765 TGCCCCAGAGAGTGTAGCCGCGACGCGATGAGACCCCTGTGAGATCTGTGGGCCATTG 824
Qy 830 GAGTCATCATATGATCATCTGTCTTTCAGGCAATCCACCTTTCTATGAGAGGTGAGAGAG 889
Db 825 GAGTCATCATATGATCATCTGTCTTTCAGGCAATCCACCTTTCTATGAGAGGTGAGAGAG 884
Qy 890 ATGATTTATGAGAACCATGATTAAGATCTCTTCCGCAAGATCTGTGGCTGTGTGATGATG 949
Db 885 ATGATTTATGAGAACCATGATTAAGATCTCTTCCGCAAGATCTGTGGCTGTGTGATGATG 944
Qy 950 TTGACTCTCATATTGGGATGATATTTCGACGAGCCAAAGACCTGTGTACAGAGCTGA 1009
Db 945 TTGACTCTCATATTGGGATGATATTTCGACGAGCCAAAGACCTGTGTACAGAGCTGA 1004
Qy 1010 TGAAGGTGAGCAAGACCGGAGATCACTGAGAGAGGCCATCTCCCATGAGTGATTT 1069
Db 1005 TGAAGGTGAGCAAGACCGGAGATCACTGAGAGAGGCCATCTCCCATGAGTGATTT 1064
Qy 1070 CTGGCAATGCTGCTTCTGATTAAGAACATCAAGATGTGTGTGTGCCAATTGAAAAA 1129
Db 1065 CTGGCAATGCTGCTTCTGATTAAGAACATCAAGATGTGTGTGTGCCAATTGAAAAA 1124
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Db 1125 ACTTTGCAAGGCGCAAGTGAAGAGGCTGTCCGAGTGACCACTCTCATGAAACGGCTCC 1184
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Db 1272 CCCCCAGCAGATGAGAGTGGCCACCCAGCCACTGATGGAGAGTTCACCCAGCCACCG 1331
Qy 1430 ATGGAACATCACTCCAGCCACTGATGGAGTTCACCCAGCTCACTGACAGAGGAGCTTA 1489
Db 1332 ATGGAACATCACTCCAGCCACTGATGGAGTTCACCCAGCTCACTGACAGAGGAGCTTA 1391
Qy 1490 CTCAGCCACTGATGGAGAGCCACACAGCCACAGAGAGAGACCTGTGCCACACACC 1549
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Qy 1550 AAACAGTGGCATGCTGGCCACCAAGGAGCTGCACTCCAGCCGAGCTATGGCCAGC 1609
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Qy 1610 CGGACAGCAGAGCCCGAGAGGAGCCACAGGCCAGCTCCACCTCTAATTAAGAGGGAGAG 1669
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Qy 1670 AGGCTGCTGTTATGCCAGAGATCTCAAAAGGAGAGGCCAGAGTGTAGAGCAGCTGG 1729
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Qy 1730 TGAGGGGGGGGAGGAGTGGGACAGAGGAGTGGAGAGTGAATGAAGGAGCTTCTCACTGA 1789
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Db 1812 GCCAGTGGAGAGGCGGCCGCCAGCCCTTGACATGATTCCTGTGGCTTTTCTGTCTTTG 1871
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Db 1932 TGCCT 1991
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Db 2352 CTCTAAGGAG 2411
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Db 2712 ATGAGAGAGTGAAGGTTAACTTCCCACTTCTGAG 2747
RESULT 10
ADB48109
ID ADB48109 standard; cDNA; 2747 BP.
XX
AC ADB48109;
XX

DT 04-DEC-2003 (first entry)
 XX Novel human cDNA SEQ ID NO 19.
 XX ss; cancer; neurodegenerative disease; human.
 XX Homo sapiens.
 XX US2003104529-A1.
 XX 05-JUN-2003.
 XX 04-JAN-2002; 2002US-00037270.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-00552317.
 XX 19-JUL-2000; 2000US-00620312.
 XX (ZHOU/) ZHOU P.
 XX (TANG/) TANG Y T.
 XX (LIUC/) LIU C.
 XX (ASUN/) ASUNDI V.
 XX (DRMA/) DRMANAC R T.
 XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
 DR MPI; 2003-678194/64.
 XX New polynucleotide, useful for treating diseases e.g., cancer or
 PT neurodegenerative diseases.
 PS Claim 1; SEQ ID NO 19; 99bp; English.
 XX The invention relates to a polynucleotide comprising a sequence given in
 CC the specification, or its mature protein-coding portion, or its
 CC complement. The polynucleotide is useful for treating diseases e.g.,
 CC cancer or neurodegenerative diseases and many others listed in the
 CC specification. The present sequence represents a novel human cDNA. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docid=20030104529.
 XX
 SQ Sequence 2747 BP; 602 A; 769 C; 801 G; 575 T; 0 U; 0 Other;
 Query Match 83.1%; Score 2595.2; DB 0; Length 2747;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

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 405 CCAAGAAAGAGATGAGATCTCAAGTGGTGAAGATCCCAATCTCAAGCTGATGG 464
 470 ATGTGTTTGTGACCCGCAAGAGACTTATCTTCTGAGCTGCGCCAGGGAGAGG 529
 465 ATGTGTTTGTGACCCGCAAGAGACTTATCTTCTGAGCTGCGCCAGGGAGAGG 524
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Db 1141 ATGAAACGGCTCCGGGCAACAGAGAGTCCAGCAGGCTGACAGCCCACTGGGCTCAAGCC 1200
QY 1237 ACAGACACTGCAACCCCGGGCTGCAAGTGGGCGCAGACGCTGACGAGTGGAGCT 1296
Db 1201 ACAGACACTGCAACCCCGGGCT----- 1224
QY 1297 ACCTCAGCCCTGAGGGTGAATGCTGTCTGTCGAAAGATGATATGTGCCCCCGCA 1356
Db 1225 -----GCA 1227
QY 1357 GACCTGAGTCCACCCCAACCCCAAGATGGAGTGCACCCCACTGATGGAGAGTGC 1416
Db 1228 GACCTGAGTCCACCCCAACCCCAAGATGGAGTGCACCCCACTGATGGAGAGTGC 1287
QY 1417 ACCCGACCAACGATGGAGATCACTCCAGCCACTGATGGAGTGCACCCCACTGACT 1476
Db 1288 ACCCGACCAACGATGGAGATCACTCCAGCCACTGATGGAGTGCACCCCACTGACT 1347
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QY 2017 CTGAGGGGGCTCTGCTCTCTCTTCCCTTCTTGTGCTCAACATTCCTCCAGGAGG 2076
Db 1873 ----- 1872
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QY 2377 CCTGTATTGTGTTATTTCTGCTTTCGAGTCTGAGTGGGCTGGCTGATCCCT 2436
Db 1873 -----GTCCTCTGATCCCT 1887
QY 2437 GAACCTATGAGCCTCTAAGGGAAGAGAAATTAAGAGTGGCAATGAGACCTGGC 2496
Db 1888 GAACCTATGAGCCTCTAAGGGAAGAGAAATTAAGAGTGGCAATGAGACCTGGC 1947
QY 2497 AGGCAAGATGACAGCCCAAGCCAGCTGTCCAGCCTTACTGGGTCTTACCTGGGCT 2556
Db 1948 AGGCAAGATGACAGCCCAAGCCAGCTGTCCAGCCTTACTGGGTCTTACCTGGGCT 2007
QY 2557 AAAAGAGAGGCTGATTAACCTCTTGTCTTCTTATGATGCCACCTCTCAATCTCAGC 2616
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QY 2617 CCAAGTCTCTCCACCCCTAGGGGCTGTGCTGATGAGCAATATCATATCTGATTTG 2676
Db 2068 CCAAGTCTCTCTCCACCCCTAGGGGCTGTGCTGATGAGCAATATCATATCTGATTTG 2127
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QY 2737 CTCCTCTTTTCTACAGCTCATTTCTATCAGAGGCCAGGTGCTTCAAGCCATTTGAGT 2796
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QY 3037 TGCAAG 3043
Db 2488 TGCAAG 2494

RESULT 13
AAS27718/c
ID AAS27718 standard; DNA, 3915 BP.
XX AAS27718;
AC
XX
DT 07-NOV-2001 (first entry)
XX
DE DNA encoding novel signal transduction pathway protein, Seq ID 1378.
XX
XX Neutropenic; cytosolic; dermatological; immunosuppressive; tumour;
XX anti-inflammatory; anti-HIV; antibacterial; anti-inflammatory; cancer;
XX immune system disorder rheumatoid arthritis inflammatory condition.

KM organ transplant rejection; infection; hepatitis C; blood disorder;
KM sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KM chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KM cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KM reproductive system; gastrointestinal; liver disorder; AIDS; ds;
KM acquired immune deficiency syndrome.
XX
OS Homo sapiens.
XX
PN MO200154733-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001312.
XX
31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249300P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251889P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465460/50.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT diagnosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 1378; 880bp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AA526976-
CC AA527850 represent novel signal transduction pathway protein coding
CC sequences and PCR primers of the invention
XX
XX Sequence 3915 BP; 900 A; 1139 C; 1049 G; 827 T; 0 U; 0 Other;
SQ
Query Match 60.1%; Score 1876.6; DB 4; Length 3915;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 2209 CCACACCAAGCACAAGAAAGAGACATGTGCCACACACCAAGACATGCTCATCTTGCCCA 2250
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Db 2249 CCAAGGAGCTGACACCCCTGAGACCGGCTATAGGCCAGCCGAGACACAGCCCCAGAG 2190
Qy 1631 GCGCCANAGCCAGGCTCCACCTCTAGTAAAGGGGAAAGAGGTGTGTGTATAGCCAG 1690
Db 2189 GCGCCANAGCCAGGCTCCACCTCTAGTAAAGGGGAAAGAGGTGTGTGTATAGCCAG 2130
Qy 1691 AGTCTAAAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1750
Db 2129 AGTCTAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2070
Qy 1751 CAGAGGAGGAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1810
Db 2069 CAGAGGAGGAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2010
Qy 1811 CCTGCTGCTCCCAATGCCCCCAATCCAGTGGGAGCATTAAGGGGTCACGGGAGAGCA 1870
Db 2009 CCTGCTGCTCCCAATGCCCCCAATCCAGTGGGAGCATTAAGGGGTCACGGGAGAGCA 1950
Qy 1871 GTCTGCTCTCTGTGTATAGTGTGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1930
Db 1949 GTCTGCTCTCTGTGTATAGTGTGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1890
Qy 1931 AGCCCTGAGATGATTCCTGTGGCTTTTGTCTTGTAGTACTTACACAGATTTCTGT 1990
Db 1889 AGCCCTGAGATGATTCCTGTGGCTTTTGTCTTGTAGTACTTACACAGATTTCTGT 1830
Qy 1991 CCTGTGAGATGCTGTCTAGAGATACAGAGGAGCTCTGTCTCTCTCTCTCTCTCTCT 2050
Db 1829 CCTGTGAGATGCTGTCTAGAGATACAGAGGAGCTCTGTCTCTCTCTCTCTCTCTCT 1770
Qy 2051 CTTGCTCTACATTCCTCTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2110
Db 1769 CTTGCTCTACATTCCTCTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1710
Qy 2111 TTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2170
Db 1709 TTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1650
Qy 2171 CTTGACATGATGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2230
Db 1649 CTTGACATGATGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1590
Qy 2231 GTATAGAGATGAGAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2290
Db 1589 GTATAGAGATGAGAAAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1530
Qy 2291 GATATGCTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
Db 1529 GATATGCTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1470
Qy 2351 AGCTTCATTTTGTCTTCTTAAGACCTGTATTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2410
Db 1469 AGCTTCATTTTGTCTTCTTAAGACCTGTATTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1410
Qy 2411 TCTGCAATGAGGCTGCTTACCTTGAACCTCATAGGCTCTTAAGGAGAAAGAGAGCA 2470
Db 1409 TCTGCAATGAGGCTGCTTACCTTGAACCTCATAGGCTCTTAAGGAGAAAGAGAGCA 1350
Qy 2471 ATTAGAGCTGTGAGATGAGACTGTGAGAGGAGAGATCAAGCCAGACCTCAATGTCCCA 2530
Db 1349 ATTAGAGCTGTGAGATGAGACTGTGAGAGGAGAGATCAAGCCAGACCTCAATGTCCCA 1290
Qy 2531 GCTTACTGAGGCTCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2590
Db 1289 GCTTACTGAGGCTCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1230
Qy 2591 AGATGCCACCTCTCAATCTAGGCCCAATCTCTTCAACCTTAAGGAGGAGGAGGAGGAGGAG 2650

Db 1229 AGATGCCACCTCCTCAAACTCAGCCACAGTCTCTCCA-CTTAGGGGGCTTGTGTC 1171
Qy 2651 ATGGCAATTAATCTAATATCTGAATTTGAGAGTTTSCCTTTACAGGGGCAATTTTCTGCT 2710
Db 1170 ATGGCAATTAATCTAATATTTGATTTGAGAGTTTSCCTTTACAGGGGCAATTTTCTGCT 1111
Qy 2711 CAGTTCAACAATGAATGAAGAAGAACTCCCTCTTTTACAGCTCACTTCTATCAGAGGC 2770
Db 1110 CAGTTCAACAATGAATGAAGAAGAACTCCCTCTTTTACAGCTCACTTCTATCAGAGGC 1051
Qy 2771 CCAGTGTCTCAGAGCCCACTTGTGTTCTTTTCTGGGATGAGGAAGTGGTTAACT 2830
Db 1050 CCAGTGTCTCAGAGCCCACTTGTGTTCTTTTCTGGGATGAGGAAGTGGTTAACT 991
Qy 2831 CCCAGTTTCTGTAGGGAGGCTCCTGACAGGTGCCCTTTGTACAGACCTTACAGCTTG 2890
Db 990 CCCAGTTTCTGTAGGGAGGCTCCTGACAGGTGCCCTTTGTACAGACCTTACAGCTTG 931
Qy 2891 GATAGGAGCCACATTTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
Db 930 GATAGGAGCCACATTTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Qy 2951 CCTGTCATGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010
Db 870 CCTGTCATGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Qy 3011 CTGAACCTGGCAATTAACATCACCCTGCAAGCC 3045
Db 810 CTGAACCTGGCAATTAACATCACCCTGCAAGCC 776

RESULT 14
ADB94521/C
ID ADB94521 standard; DNA; 3915 BP.
AC ADB94521;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human protein DNA #130.
XX
KM ds; Gene; human; autoimmune disease; Parkinson's disease; silicosis;
KM gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KM immunosuppressive agent; adjuvant; enhance immune response;
KM higher affinity antibody induction;
KM increased serum immunoglobulin concentration.
XX
XX Homo sapiens.
OS
XX
EN US2002168711-A1.
XX
PD 14-NOV-2002.
XX
PF 17-JAN-2001; 2001US-00764868.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216547P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-022547P.
PR 14-AUG-2000; 2000US-0225475P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR

PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237033P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI WPI; 2003-719985/68.
XX
XX The invention relates to an isolated polypeptide. The polypeptide is
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in the nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents DNA encoding a novel human protein. Note: The
CC sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format direct from USPRO at
CC seqdata.uspro.gov/sequence.html?docid=20020168711.

XX Sequence 3915 BP; 900 A; 1139 C; 1049 G; 827 T; 0 U; 0 Other;

Query Match 60.1%; Score 1876.6; DB 9; Length 3915;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 1151 AGAAGGCTGTCGAGAGACCAACCTCATGAAACGGCTCCGGGACACCAAGAGCTCCAGCA 1210
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QY 1331 CAAAGGTATATATGTGGCCCCCGCAGACCGTATGTGCCACCCAGCCACAGATGGAATG 1390
DB 2489 CAAAGGTATATATGTGGCCCCCGCAGACCGTATGTGCCACCCAGCCACAGATGGAATG 2430
QY 1391 CCAAGGCTGCAAGTGGGAGTGAAGTAACTCCTCAGCCCTGAGGGTGAAGCTGCTGCTG 1450
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QY 1451 CTGATGGAGTGTCAACCCAGTCACTGACAGAGGCTTACTCAGCACTGATGGAGAG 1510
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DB 2249 CCAAGGCTGCAAGTGGGAGTGAAGTAACTCCTCAGCCCTGAGGGTGAAGCTGCTGCTG 2190
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DB 2069 CAGAGAGGTGGAGAGTGAATGAAGGGCTTCTCACTGTATAGATCACTGGCATATG 2010
QY 1811 CCTGTGCTCCCATGCCCCCACAATCCAGTGGGGATAACTAGGGGTAGAGGGGAGAGA 1870
DB 2009 CCTGTGCTCCCATGCCCCCACAATCCAGTGGGGATAACTAGGGGTAGAGGGGAGAGA 1950
QY 1871 GTCTGTCTCTGTGTATGTGTAGTGTGAGTGTGGCAGAGCCAGTGGCAGAGCCGCC 1930
DB 1949 GTCTGTCTCTGTGTATGTGTAGTGTGAGTGTGGCAGAGCCAGTGGCAGAGCCGCC 1890
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DB 1889 AGCCCTGATGATGATTTCTTGTGCTTTTGTGCTTTTGTAGCTTACCAAGTTTCTGT 1830
QY 1991 CCTGTGAGGATGCTGCTCTAGAGATACAGAGGGGCTCCTGCTCTCTTCCCTTCCCTT 2050
DB 1829 CCTGTGAGGATGCTGCTCTAGAGATACAGAGGGGCTCCTGCTCTCTTCCCTTCCCTT 1770
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QY 2171 CCTGCATATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2230
DB 1649 CCTGCATATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1590
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DB 1409 TCCGCAAGTGGGCGCCCTGTAACCTGAACTGATGAGCTTAAGGGAAAGAGAGACA 1350
QY 2471 ATTAGAGAGTGGCAATGAGACCTGCGAGGGCAGAGTAAAGCCAGCAGCCAGTGTCCA 2530
DB 1349 ATTAGAGAGTGGCAATGAGACCTGCGAGGGCAGAGTAAAGCCAGCAGTGTGTCCA 1290
QY 2531 GCTTACTGAGGCTTACCTGAGGCGCAACAGAGAGGAGGCTGATATCTTCTTCTTCT 2590
DB 1289 GCTTACTGAGGCTTACCTGAGGCGCAACAGAGAGGAGGCTGATATCTTCTTCTTCT 1230
QY 2591 AGATGCCCACTCTCTAATCTCAGGCCACAAGTCTCTCTCAACCTTGAAGGGGCTTGTGC 2650
DB 1229 AGATGCCCACTCTCTAATCTCAGGCCACAAGTCTCTCTCAACCTTGAAGGGGCTTGTGC 1171
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DB 1170 ATGGCAATTAATCTAATATGATTTGAGAGGTTGCTTCAAGGGGCAATTTTCTGCT 1111
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DB 990 CCCAGTTTCTGAGGAGAGGCTCTGACAGTGCCCTTGTGACACCTTACACAGGCTG 931
QY 2891 GATAGGAGCCACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
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DB 810 CTGAACCTGGCAATTAACATCACTGCAAGGC 776
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RESULT 15

ABA95683 standard; DNA; 7542 BP.

ABA95683;

03-APR-2002 (first entry)

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DE Human protein kinase gene.
XX
XX Human; protein kinase; enzyme; gene; brain; lung; hippocampus;
KW calmodulin-binding kinase; gene therapy; chromosome 3;
XX single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key
FH Location/Qualifiers
FH variation
FT /tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT /replace(328,C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT /replace(1473,.4544)
FT /tag= c
FT /product= "Human protein kinase"
FT /transl_except= (pos:4275..4277, aa:Val)
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FT /number= 1
FT /replace(1499,T)
FT /tag= e
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FT /replace(1568,.1684)
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FT /tag= q
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FT /replace(3295,T)
FT /tag= t
FT /standard_name= "Single nucleotide polymorphism"
FT /replace(3313,.3391)
FT /tag= u
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FT /number= 9
FT /tag= y
FT /number= 10
FT /replace(14677,T)
FT /tag= z
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FT /replace(5583,Y)
FT /tag= aa
FT /standard_name= "Single nucleotide polymorphism"
FT /replace(6242,C)
FT /tag= ab
FT /standard_name= "Single nucleotide polymorphism"
FT /replace(7264,G)
FT /tag= ac
FT /standard_name= "Single nucleotide polymorphism"
XX
XX WO200192492-A2.
XX
XX PN
XX
XX PD
XX
XX PP
XX
XX PR
XX
XX PR
XX
XX PR
XX
XX PA
XX
XX PI
XX
XX PI
XX
XX DR
XX
XX DR
XX
XX PS
XX
XX
XX The present sequence is a human protein kinase gene. The protein kinase
XX coding sequence (see ABA95682) is expressed in the brain (both infant and
XX adult brain), lung and hippocampus. The protein kinase is related to the
XX calmodulin-binding kinase subfamily. The protein kinase and its coding
XX sequence can be used as models for the development of human therapeutic
XX targets, in the identification of human therapeutic agents, and serve as
XX kinase activity in cells and tissues that express the kinase. In
XX addition, the protein kinase coding sequence can be used for treating a
XX disorder associated with nucleic acid expression of the kinase gene,
XX particularly biological and pathological processes that are mediated by
XX the kinase in cells and tissues that express it, as antisense constructs
XX to control kinase gene expression in cells, tissues or organisms, and in
XX gene therapy. The protein kinase gene maps to chromosome 3
XX
XX SO
XX Sequence 7542 BP; 1612 A; 1977 C; 2156 G; 1797 T; 0 U; 0 Other;
XX
XX
XX Query Match
XX Best Local Similarity 60.1%; Score 1876.6; DB 6; Length 7542;
XX Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
XX
XX
XX 1151 AGAAGGCTGTCCGAGTACACCCCTCAATGAACGCTCCGGGACACAGAGTCCAGCA 1210
XX |||||
XX 3979 AGAAGGCTGTCCGAGTACACCCCTCAATGAACGCTCCGGGACACAGAGTCCAGCA 4038
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QY	1211	GGGCTGCGACGCCGAGTGGGGCTTACGCCACAGACATGCGCACCCCGGGGGCTGGACAGTGGGG	1270
Db	4039	CGGCTCAGCCCGAGTGGGGCTTACGCCACAGACATGCGCACCCCGGGGGCTGGAGTGGGG	4098
QY	1271	CCACACTGCAGGTGGAGTGGAGTCACTCAGCCCTTAGAGGGTGAATGCTGCTGCTG	1330
Db	4099	CCACACTGCAGGTGGAGTGGAGTCACTCAGCCCTTAGAGGGTGAATGCTGCTGCTG	4158
QY	1331	CAAAAGTGAATTAATGCGCCCGCAGACCGTAAATGTCACCCGCAAGATGGAATG	1390
Db	4159	CAAAAGTGAATTAATGTCGCCCGCGCAGACCGTGAATGCCACCCGACAGATGGAATG	4218
QY	1391	CCACCCCAAGCACTGAATGGAGATGTCAACCCCAAGCCCAATGGAAACATCACTCCAGCCA	1450
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QY	1511	CCACACCAAGCCACAGAGAGAGCACTGTGCCACCAACCCAAAGCAGTGCATCTGGCCA	1570
Db	4339	CCACACCAAGCCACAGAGAGAGCACTGTGCCACCAACCCAAAGCAGTGCATCTGGCCA	4398
QY	1571	CCAAAGCAGTGCACCCCTGAGACCGGCTATGGCCAGCCGGACAGCAGCCCCAGAG	1630
Db	4399	CCAAAGCAGTGCACCCCTGAGACCGGCTATGGCCAGCCGGACAGCAGCCCCAGAG	4458
QY	1631	GGCGCACAGGCCAGAGCTCCACCCCTCTAGTAAAGGGGAAAGGCTGCTGCTTATGCCAG	1690
Db	4459	GGCGCACAGGCCAGAGCTCCACCCCTCTAGTAAAGGGGAAAGGCTGCTGCTTATGCCAG	4518
QY	1691	AGTCTCAAAGGAGAGAGCCAGCTGAGTAGAGCCTGTGAGAGGGGGAGAGGGGAATGG	1750
Db	4519	AGTCTCAAAGGAGAGAGCCAGCTGAGTAGAGCCTGTGAGAGGGGGAGAGGGGAATGG	4578
QY	1751	CAGAGGGGTGGAGAGTGTGATGAGGGGCTTCTACTGTACATAGATCACTGGCATGATG	1810
Db	4579	CAGAGGGGTGGAGAGTGTGATGAGGGGCTTCTACTGTACATAGATCACTGGCATGATG	4638
QY	1811	CCCTGCGTCCGCCCATGCCCCCACTGCCAGTGGGGCACTAACTAGGGGTCACGGAGAGCA	1870
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QY	1871	GTCCTGCTCTCTGTGTGTATGTGTGTAGTGTGGAGAGCCAGTGGCAGGGCCGAGCCC	1930
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QY	1991	CCTTGTGGGATGCGTCTAGGAACTACAGGGGGGCTCCTGCTCTCCCTCCCTCCCT	2050
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QY	2111	TTGGGCGGCGCTTGGCTGAGAGCTGTCTTCACAGAGGCCCTGTCAAGGCTCTTAAGCT	2170
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QY	2171	CCTGCACTGAAGGTGTGCTGCTGGTGTGTGGGCTGCTCTTAGAGCAGATACAGGCTG	2230
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QY	2231	GTATAGAGATGACAAAGATAGGCGAGTATGTTAATCCAGACTTGGCAGATGGCTAG	2290
Db	5059	GTATAGAGATGACAAAGATAGGCGAGTATGTTAATCCAGACTTGGCAGATGGCTAG	5118
QY	2291	GGATATCTGCTCACTAGCTGTGAGGTCTCTCAGAGTGGAGAAATAGTACAGAGCGCAGA	2350

Db	5119	GGATTAATGCTCACTACCTGCTGAGAGGTCTCAGSAGTGGAGAGAAATAGATAGAGGGGAGA	5178
QY	2351	AGCTTCATTTTGTGCTTCTCTTAAGACCCGTATTTGTGTATTTTCCTGCTTCCGAG	2410
Db	5179	AGCTTCATTTTGTGCTTCTCTTAAGACCCGTATTTGTGTATTTTCCTGCTTCCGAG	5238
QY	2411	TCTCGAATGGGCTGGCCCTGATACCCGAAACCTCATAGACCTCTAAAGGAAAGAGAGACA	2470
Db	5239	TCTCGAATGGGCTGGCCCTGATACCCGAAACCTCATAGACCTCTAAAGGAAAGAGAGACA	5298
QY	2471	ATTAGGACGTGGGCAATGAGACCTCGGAGGGCAGAGTAAACAAGCCAGACCCAGTGTCCA	2530
Db	5299	ATTAGGACGTGGGCAATGAGACCTCGGAGGGCAGAGTAAACAAGCCAGACCCAGTGTCCA	5358
QY	2531	GCCTTACTGGTCTCTTACCCTGGGCAAAACAGGAGGGCTGATACCTCTTGTCTTCT	2590
Db	5359	GCCTTACTGGTCTCTTACCCTGGGCAAAACAGGAGGGCTGATATACCTCTTGTCTTCT	5418
QY	2591	AGATGCCACCTCTCAACATCTGAGCCACAGTCTCTTCAACCTTAGGGGCTTGTCTGC	2650
Db	5419	AGATGCCACCTCTCAACATCTGAGCCACAGTCTCTCA-CTTAGGGGCTTGTCTGC	5477
QY	2651	ATGGCAATTAATCTATATCTGATTTTGGAGTTTGGCTTTTACAGGGGCAATTTTCTGCT	2710
Db	5478	ATGGCAATTAATCTATATTTGATTTTGGAGTTTGGCTTTTACAGGGGCAATTTTCTGCT	5537
QY	2711	CAGTTCAACATGAATGAAGAGAACTCCCTCTTTTACAGCTCACTTCTATCAGAGGC	2770
Db	5538	CAGTTCAACATGAATGAAGAGAACTCCCTCTTTTACAGCTCACTTCTATCAGAGGC	5597
QY	2771	CCAAGTGCCTCAGAGCCACATTGATGTTCTTTTCTGGATGAGAAATGAGGTTAACT	2830
Db	5598	CCAAGTGCCTCAGAGCCACATTGATGTTCTTTTCTGGATGAGAAATGAGGTTAACT	5657
QY	2831	CCCCAGTTTCTGAGGAGGCTCTCTGACAGGTGCCCTTTGTCAAGCCTTACACAGCTG	2890
Db	5658	CCCCAGTTTCTGAGGAGGCTCTCTGACAGGTGCCCTTTGTCAAGCCTTACACAGCTG	5717
QY	2891	GATAGGAGGCACATTGTCTCTGCGCCCTTCTCGGACCTCCGATGTGCTCTGCGCCCT	2950
Db	5718	GATAGGAGGCACATTGTCTCTGCGCCCTTCTCGGACCTCCGATGTGCTCTGCGCCCT	5777
QY	2951	CCCGTCATGCTGTGGGTGCTGTGTGTGTAAGTCCGGTGGTTAACTGTGTGCTTA	3010
Db	5778	CCCGTCATGCTGTGGGTGCTGTGTGTGTAAGTCCGGTGGTTAACTGTGTGCTTA	5837
QY	3011	CTGAACCTGGCAATTAACATCACTCTGCAAGCC	3045
Db	5838	CTGAACCTGGCAATTAACATCACTCTGCAAGCC	5872

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